

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 18, 2004, 10:04:46 : Search time 2818 Seconds
(without alignments)
18881.523 Million cell updates/sec

Title: US-10-016-248-1
Perfect score: 10136
Sequence: 1 atgcgcggcgccctccccc.....ctcagcgcgccacgcgcac 10136

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

N_Geneseq_23Sep04*
1: geneseqn1980s:*
2: geneseqn1990s:*
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4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
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8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	10136	100.0	10136	6	ABSG64375 Human club
2	10136	100.0	10136	12	ADH71137 Human gen
3	10134.4	100.0	10136	12	ADH71165 Human gen
4	10132.8	100.0	10136	12	ADH71167 Human gen
5	9710.4	95.8	9951	12	ADH71141 Human gen
6	9508	93.8	10655	12	ADH71135 Human gen
7	9120	90.0	10466	12	ADH71143 Human gen
8	8760.4	86.4	12900	12	ADH71145 Human gen
9	7616.4	75.1	8010	12	ADH71139 Human gen
10	7614.8	75.1	8004	6	ABSG64376 Human club
11	4260.4	42.0	6004	6	AA149944 Human mol
12	4183.2	41.3	12525	6	AAAD33319 Human C3b/C
13	4174.2	41.2	10989	12	ADH72215 Human gen
14	4067.4	40.1	10433	6	AAAD33320 Human C3b
15	4067.4	40.1	10673	6	AAAD33318 Human C3b
16	3597.8	35.5	3896	4	AAAF87127 Human cod
17	3597.8	35.5	3896	12	ADH71163 Human gen
18	3561.8	35.1	3905	4	AAAF87126 Human cod
19	3549.8	35.0	3904	12	ADH71161 Human gen
20	2716	26.8	8034	6	AAAS18806 DNA encod
21	2715.4	26.8	7333	6	AAAS18805 DNA encod

22	2671	26.4	6409	6	AAAS18803 DNA encod
23	2595	25.6	2607	12	ADH71153 Human gen
24	2503.6	24.7	5598	6	AAAS18801 DNA encod
25	2482.6	24.5	2997	10	ADG30517 Human nov
26	2450.8	24.2	5667	6	AAAS18804 DNA encod
27	2450.2	24.2	6145	6	AAAS18802 DNA encod
28	2331	22.8	2328	12	ADH71149 Human gen
29	2303	22.7	2329	12	ADH71147 Human gen
30	2122.4	20.9	2487	4	AAAS00146 Human cdn
31	1919.8	18.9	2132	12	ADH71151 Human gen
32	1776.8	17.5	1792	12	ADH71157 Human gen
33	1569	15.5	3810	11	ADM02129 Human cdn
34	1442.8	14.2	4506	6	ABSS58378 Protein m
35	1371.6	13.5	2387	6	ABAN9361 Human sec
36	1031.2	10.2	1615	6	ABA00063 CADHP-10
37	978.4	9.7	2026	10	ADC30413 Human nov
38	954.2	9.4	3019	12	ADH72219 Human gen
39	852	8.4	1749	10	ADC30885 Human nov
40	796.2	7.9	3117	8	ABX34721 Human int
41	783.6	7.7	2609	6	AAD37600 Human int
42	733.8	7.2	1135	4	AAAF83001 Human mbs
43	733.8	7.2	1135	12	ADH71159 Human gen
44	594.8	5.9	894	8	ACD05597 DNA enco
45	585.4	5.8	3145	8	ABX72185 Human NOV

ALIGNMENTS

RESULT 1	ABSG64375	standard; DNA; 10136 BP.
ID	ABSG64375	
XX	ABSG64375;	
XX	15-NOV-2002 (first entry)	
XX	Human club and sushi domain containing gene #1.	
XX	Human; NOVX; neurodegenerative disease; Alzheimer's disease; anxiety;	
KW	Parkinson's disease; Huntington's disease; neurological disorder;	
KW	Schizophrenia; manic depression; mental retardation; angina pectoris;	
KW	cardiovascular disease; acute heart failure; myocardial infarction;	
KW	muscular disease; muscular disorder; retinal disease; photoreception;	
KW	deafness; keratinisation disorder; cancer; ovarian cancer; melanoma;	
KW	immunological disorder; inflammatory disease; immune disease; diabetes;	
KW	bacterial infection; fungal infection; protozoal infection; obesity;	
KW	viral infection; reproductive system disorder; metabolic disturbance;	
KW	anorexia; wasting disorder; chronic disease; infectious disease;	
KW	dyslipidaemia; club; sushi; myelin; von Willebrand factor; kielin;	
KW	semaphorin; serine/threonine protein kinase; TGF-beta binding;	
KW	mas proto-oncogene; ribonuclease pancreatic precursor; aminotransferase;	
KW	collid-like 2; cysteine sulfonic acid decarboxylase; gene; ds;	
KW	single nucleotide polymorphism; SNP.	
OS	Homo sapiens.	
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PR	15-MAY-2001;	2001US-0291037P.
PR	08-JUN-2001;	2001US-0297173P.
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PR	29-AUG-2001;	2001US-0315639P.
PR	01-OCT-2001;	2001US-0326393P.
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PI	Guo X, Herrmann JI, Kekuda R, Lepley DM, Li L, MacDougall JR,	
PI	Millet I, Pena CE, Peyman JA, Rastelli L, Rieger DK, Shinkets RA,	
PI	Smithson G, Sytek KM, Stone DJ, Tchernov VT, Vernet CM, Voss EZ,	
XX	Zerhusen BD, Zhong H, Zhong M,	
DR	WPI; 2002-643486/69.	
XX	P-SDB; ABC79168.	
PT	New NOVX polypeptides and polynucleotides useful for treating or	
PT	preventing e.g. neurodegenerative diseases, neurological disorders,	
PT	cardiovascular diseases, muscular diseases and disorders, or	
PT	immunological diseases.	
XX		
PS	Claim 9: Page 10-12; 299pp; English.	
XX		
CC	The present invention relates to new NOVX polypeptides. The polypeptides,	
CC	polynucleotides and antibodies are useful in the manufacture of a	
CC	medicament for treating or preventing neurodegenerative diseases (e.g.	
CC	Alzheimer's disease, Parkinson's disease, or Huntington's disease).	
CC	neurological disorders (e.g. anxiety, schizophrenia, manic depression or	
CC	mental retardation), cardiovascular disease (e.g. acute heart failure,	
CC	angina pectoris or myocardial infarction), muscular diseases and	
CC	disorders, retinal diseases (including those involving photoreception,	
CC	deafness and keratinisation disorders), cancer (e.g. ovarian cancer or	
CC	melanoma), immunological disorders, inflammatory and immune diseases,	
CC	bacterial, fungal, protozoal and viral infections, and reproductive	
CC	system disorders. The proteins of the invention may be used to screen	
CC	drugs or compounds that modulate the NOVX protein activity or expression,	
CC	as well as to treat disorders characterised by insufficient or excessive	
CC	production of NOVX protein or protein forms that have decreased or	
CC	aberrant activity compared to NOVX wild type protein, such as diabetes,	
CC	obesity, metabolic disturbances associated with chronic diseases and	
CC	wasting disorders associated with chronic diseases and various cancers,	
CC	infectious diseases and various dyslipidaemias. The nucleic acid	
CC	sequences of the invention may be used in chromosome mapping, identifying	
CC	an individual from minute biological samples (tissue typing), and in	
CC	forensic identification of a biological sample. The present nucleic acid	
CC	sequence encodes a NOVX protein of the invention	
XX		
SQ	Sequence 10136 BP; 2147 A; 3060 C; 2744 G; 2185 T; 0 U; 0 Other;	
Query Match	100.0%; Score 10136; DB 6; Length 10136;	
Best Local Similarity	100.0%; Pred. No. 0;	
Matches 10136;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
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Db	121 GAGTTGAAGTCTCGAGGTGTGAAGCTGATGCCAGAAAGACAAACAGCAAGAGCTGT 180	

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Qy	1141	GACATTGACGTGAGGCTCAGTTGATTTCTGTGTCATCAAGATGGGGCCACCGCGAG	1200
Db	1141	GACATTGACGTGAGGCTCAGTTGATTTCTGTGTCATCAAGATGGGGCCACCGCGAG	1200
Qy	1201	GCGGCGGCTCTGGGCACTTTCTAGGAAACCACTTCTCTCTTCATCAACAGATGGC	1260
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DB 9961 TGTGCAAGAGATTAACCAACCGGCTGGCGCTTTTGTGAGTGAATGTGACT 10020
QY 10021 CCAAGACCGCGAAGCTGAGACTGTACTGTGCTCATCTCAGCTCACTGCAACTCCCTGC 10080

Seq	Sequence	10136 BP; 2147 A; 3060 C; 2744 G; 2185 T; 0 U; 0 Other;
Query Match	100.0%; Score 10136; DB 12; Length 10136;	
Best Local Similarity	100.0%; Pred. No. 0;	
Matches 10136; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 ATGGCGGGGCGCCCTCCCGCCCGCTGTGTGCTGCTTGAGTTGATCTCAGCTCTGT	60
DB	1 ATGGCGGGGCGCCCTCCCGCCCGCTGTGTGCTGCTTGAGTTGATCTCAGCTCTGT	60
QY	61 GCTAGCAATCAGCGCACTCCGTGGGCGTAGAGACCTCCAGGTAGTCAAGAACAAATT	120
DB	61 GCTAGCAATCAGCGCACTCCGTGGGCGTAGAGACCTCCAGGTAGTCAAGAACAAATT	120
QY	121 GAGTTGAAGTCTCGAGGTGTGAAGTCAATGCCGACAAAGCAACCAAGCAAGAGCTGT	180
DB	121 GAGTTGAAGTCTCGAGGTGTGAAGTCAATGCCGACAAAGCAACCAAGCAAGAGCTGT	180
QY	181 GTGTTAACTCAGGTGTGTGTCTCCAAAGCATATATGTGTCCAGACCTGGCATATCC	240
DB	181 GTGTTAACTCAGGTGTGTGTCTCCAAAGCATATATGTGTCCAGACCTGGCATATCC	240
QY	241 GAAAGGGGCAAAAGCTTAGGCTCGGATTTTCAAGTTAGATCCAGCCTCAATTCCTGC	300
DB	241 GAAAGGGGCAAAAGCTTAGGCTCGGATTTTCAAGTTAGATCCAGCCTCAATTCCTGC	300
QY	301 AACGAGGGCTATGACTCTGCAAGGGTCCAGCGGATCACTGTATGAAAGTGAAGCAATG	360
DB	301 AACGAGGGCTATGACTCTGCAAGGGTCCAGCGGATCACTGTATGAAAGTGAAGCAATG	360
QY	361 TTTGGGGCTTGAGAGCAACACAGGCCGATGTCCCGAGCCCGCATGTGTATGCCACCTT	420
DB	361 TTTGGGGCTTGAGAGCAACACAGGCCGATGTCCCGAGCCCGCATGTGTATGCCACCTT	420
QY	421 CGAGGCCCTTGAGGCTATCACTCCCGCAATTTCCCATTCAGATGACAAATATCA	480
DB	421 CGAGGCCCTTGAGGCTATCACTCCCGCAATTTCCCATTCAGATGACAAATATCA	480
QY	481 CACTGTGTGTGATCATCAAGCACTCAACCCCTCCAGATGATCAAGCTCGCTTTGAG	540
DB	481 CACTGTGTGTGATCATCAAGCACTCAACCCCTCCAGATGATCAAGCTCGCTTTGAG	540
QY	541 GAGTTGATTTGAGAGGGGCTATGACACCTCTGAGGTGGATGTGTGATGATGAGATGG	600
DB	541 GAGTTGATTTGAGAGGGGCTATGACACCTCTGAGGTGGATGTGTGATGATGAGATGG	600
QY	601 GACCAAGAACAGTTCTTCAATGTCTCAAAATCCTGTGACGTGACAGCCCTCAACCCCA	660
DB	601 GACCAAGAACAGTTCTTCAATGTCTCAAAATCCTGTGACGTGACAGCCCTCAACCCCA	660
QY	661 GGCTCTGCAATCCAGAGAGCATGTCTGGGAGCATTTGAGAGCAGAAATGAGATCTACTT	720
DB	661 GGCTCTGCAATCCAGAGAGCATGTCTGGGAGCATTTGAGAGCAGAAATGAGATCTACTT	720
QY	721 GAGATCTGTGTGATCATTTAGCATTTGAGATGCAAGGTCAAGTTTCAAGTGAAGAGTCTCA	780
DB	721 GAGATCTGTGTGATCATTTAGCATTTGAGATGCAAGGTCAAGTTTCAAGTGAAGAGTCTCA	780
QY	781 AAGCTTTCTAATGCTGTGGAACCTTTGTCTCTGGGACAGAGATGAGCAGGGCAGTTTC	840
DB	781 AAGCTTTCTAATGCTGTGGAACCTTTGTCTCTGGGACAGAGATGAGCAGGGCAGTTTC	840
QY	841 GGTGACCTTGGCATATCTGTGATTTGACCGGAGAGAGAGGTCCCGGTTTCAACAGGGTAC	900
DB	841 GGTGACCTTGGCATATCTGTGATTTGACCGGAGAGAGAGGTCCCGGTTTCAACAGGGTAC	900
QY	901 ACACTCAAGTTTGAATGCCAGCCCGCTTTGAGCTGTGGACAGAAAGCAATCATATGC	960
DB	901 ACACTCAAGTTTGAATGCCAGCCCGCTTTGAGCTGTGGACAGAAAGCAATCATATGC	960
QY	961 CAAAAGATTAACCAAGTCCGTTAAGAGCAAGGCTCGATTCTCTGTTCTTTAC	1020
DB	961 CAAAAGATTAACCAAGTCCGTTAAGAGCAAGGCTCGATTCTCTGTTCTTTAC	1020

QY	1021	TTACACGAGCCGGTCTGAGGGTGTGCTGTCTCCGCACTACACCGAGAGACATATGGCAACAC	1087
Db	1021	TTTACACAGCCCGGTCTGAGGGTGTGCTGTCTCCCACTACACCGAGAGACATATGGCAACAC	1080
QY	1081	CTTCACTGTGTGTGAGCTCATCTTGGCCAGGCTGTAGAGCCGATCACCTGGCTTTTCAAC	1144
Db	1081	CTTCACTGTGTGTGAGCTCATCTTGGCCAGGCTGTAGAGCCGATCACCTGGCTTTTCAAC	1144
QY	1141	GACATTGAGCTGAGAGCTTCAAGTTTGAATTTCTGTGTATCAAGATGGGGCCACCGCCGAG	1200
Db	1141	GACATTGAGCTGAGAGCTTCAAGTTTGAATTTCTGTGTATCAAGATGGGGCCACCGCCGAG	1200
QY	1201	GGGCCCGTCTGGGGACCTTCCAGGAAACAGCTTCCCTCTCATACACAGAGTGGC	1266
Db	1201	GGGCCCGTCTGGGGACCTTCCAGGAAACAGCTTCCCTCTCATACACAGAGTGGC	1266
QY	1261	CACGTGGCCCTGTCTGAAGTTCCAGCTGACACTTCCACAGGGAAGAGGGGCTTCAACATC	1320
Db	1261	CACGTGGCCCGTCTGAGTTCCAGCTGACACTTCCACAGGGAAGAGGGGCTTCAACATC	1320
QY	1321	ACTTTTACACCTTCCGACACACAGAGTGGCCGAGTCCGTGGCGTTCCAGTAAATGGCAA	1380
Db	1321	ACTTTTACACCTTCCGACACACAGAGTGGCCGAGTCCGTGGCGTTCCAGTAAATGGCAA	1380
QY	1381	CGGTTTGGGGACAGCCTTCCAGCTGGGACGTCATCTTCTCTGTGATGAAGGCTTC	1440
Db	1381	CGGTTTGGGGACAGCCTTCCAGCTGGGACGTCATCTTCTCTGTGATGAAGGCTTC	1440
QY	1441	CTTGGGACCTCAGGGGCTCAGAGACCATCACTGGCTCTGAAAGAGGGCAGCGTGTCTGG	1500
Db	1441	CTTGGGACCTCAGGGGCTCAGAGACCATCACTGGCTCTGAAAGAGGGCAGCGTGTCTGG	1500
QY	1501	AACAGCGCTGTGCTGGCGTGTGAAGCTCCCTGTGTGGTCACTGACCTTCCGCCAGCGGC	1560
Db	1501	AACAGCGCTGTGCTGGCGTGTGAAGCTCCCTGTGTGGTCACTGACCTTCCGCCAGCGGC	1560
QY	1561	ACCATCTCTCTCTCGGGGCTGGCGCTTGTCTTACAAGATGCTTGAAGCTGTGCTGGGCTG	1620
Db	1561	ACCATCTCTCTCTCGGGGCTGGCGCTTGTCTTACAAGATGCTTGAAGCTGTGCTGGGCTG	1620
QY	1621	ATTGAGGCCACGACGAGCTACCCCATCAAAATCACTTCCAGACATTCACAAACCGAGAGTC	1680
Db	1621	ATTGAGGCCACGACGAGCTACCCCATCAAAATCACTTCCAGACATTCACAAACCGAGAGTC	1680
QY	1681	AACATATGACACTTGGAAATACGGGATGGGCGGACTTACTCAGGCGCTTGTATGGGGTT	1740
Db	1681	AACATATGACACTTGGAAATACGGGATGGGCGGACTTACTCAGGCGCTTGTATGGGGTT	1740
QY	1741	TACACCGGGAACGAGGTTCCCAATTCCTATACAGCACAGCAACTACCTTACCTCTC	1800
Db	1741	TACACCGGGAACGAGGTTCCCAATTCCTATACAGCACAGCAACTACCTTACCTCTC	1800
QY	1801	TTCTCTTACCGACAAAGATCACTGGGACATCGGCTTCCAGCTCGCTATAGACTATAC	1860
Db	1801	TTCTCTTACCGACAAAGATCACTGGGACATCGGCTTCCAGCTCGCTATAGACTATAC	1860
QY	1861	CTTGAGTCAACACCATGTCTGTGATCCAGGAATCCAGTAAATGACAGCTCATGGGAAT	1920
Db	1861	CTTGAGTCAACACCATGTCTGTGATCCAGGAATCCAGTAAATGACAGCTCATGGGAAT	1920
QY	1921	GACTTCTACGAGGGCGGCTGTGATGACTTACAGCTGTGACTCGGGCTTACACATTAAAGTAC	1980
Db	1921	GACTTCTACGAGGGCGGCTGTGATGACTTACAGCTGTGACTCGGGCTTACACATTAAAGTAC	1980
QY	1981	GGGAGCCTTGGAGTGTAGGCCCACTTCCAGTGGACCGGGCCCTGGCCCAAGTTGTGA	2040
Db	1981	GGGAGCCTTGGAGTGTAGGCCCACTTCCAGTGGACCGGGCCCTGGCCCAAGTTGTGA	2040
QY	2041	GCCTCTGAGGTGGCTTCAATTAAGGCTCAGATGGGACCATCTTGTGCGCAGGGTTCCT	2100
Db	2041	GCCTCTGAGGTGGCTTCAATTAAGGCTCAGATGGGACCATCTTGTGCGCAGGGTTCCT	2100

QY 2101 GACCTTACCCCAACAATTGAATGCACTGATTAATGAAACATCTCATGGCAAGGT 2160
DB 2101 GACTTACCCCAACAATTGAATGCACTGATTAATGAAACATCTCATGGCAAGGT 2160
QY 2161 GTGTTCTTCACTTTCCACACTTTCACTGGAAGTGGCCATGACTTCTCTCATCT 2220
DB 2161 GTGTTCTTCACTTTCCACACTTTCACTGGAAGTGGCCATGACTTCTCTCATCT 2220
QY 2221 GGAAGAGGAGCTTCAACCCAGCCCTGAGGAGCTGAATGATGCTGGGCTGCAAGTCCC 2280
DB 2221 GGAAGAGGAGCTTCAACCCAGCCCTGAGGAGCTGAATGATGCTGGGCTGCAAGTCCC 2280
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DB 2521 GGGCAGACGGCGCTGTGAGAGCTTCCCTGCAAGGTGTGTGCTGAGTGTGGAAATTCA 2580
QY 2581 GTTACAGGCACTACGGGTACTTGTGCTGTCCCAACTTTCCTGTGAATCAATCAATCAAT 2640
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DB 2641 CATGAATGATCTACTCTCACTCCAGACCCAGGAGGAGAAATTGAGTGAAGCCAGG 2700
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DB 2941 AAGGTTCAATGATGAAGTCAATTTTGAAGGAGGAGTCCGTGCTTCACTGTGACCTTGA 3000
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DB 3001 TACAGGCTGAGGAGTGTGAGAGAGTGTGTCTGATGAGGAGGAGGAGGAGGAGCTGGAG 3060
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DB 3181 ATGGAAGCAGAGGCGGCTGCAACATTTGGGCTACACTTCTGTGTTTGAACAGAGAG 3240
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DB 3841 GGCAGGATGGAAG 3900
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DB 3961 GGTTCATCAAG 4020
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Db 7021 TGTGACCTGTGCTACTATCTACTGTGCAAAAGGCTATCCGCTGTAGGCGCAATGGCAAA 7080
QY 7081 TGGAGCTCGGGGACTCTACGCCCACTGCGAATCATCTCTGTGAGAGCTCCGAT 7140
Db 7081 TGGAGCTCGGGGACTCTACGCCCACTGCGAATCATCTCTGTGAGAGCTCCGAT 7140
QY 7141 CCCCCCAATGGCCACCGGCACTGGGAACACTGTCTGTCTACGGGGCAACAGCATCTTCTCC 7200
Db 7141 CCCCCCAATGGCCACCGGCACTGGGAACACTGTCTGTCTACGGGGCAACAGCATCTTCTCC 7200
QY 7201 TGGCAATTCGGATACACACTGTGGGCTCCAGGGTGGTGTGATGCAATGGGCAATGGGCTC 7260
Db 7201 TGGCAATTCGGATACACACTGTGGGCTCCAGGGTGGTGTGATGCAATGGGCAATGGGCTC 7260
QY 7261 TGGAGTGGCTCTGAGAGTCCGCTGCTGTGAGCACTGTGAGCACTCTGAGCCATTTGTC 7320
Db 7261 TGGAGTGGCTCTGAGAGTCCGCTGCTGTGAGCACTGTGAGCACTCTGAGCCATTTGTC 7320
QY 7321 AACGGACACATGAATGGGGAACCTACAGTACCGGGGCAAGTGTGTATACCAATGCAT 7380
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QY 7381 GGTGCTTCGCTGATCGGATGTCTGTGCGGATCTGCGAGAGGATCATCACTGGTGG 7440
Db 7381 GGTGCTTCGCTGATCGGATGTCTGTGCGGATCTGCGAGAGGATCATCACTGGTGG 7440
QY 7441 GGGCAAGCCCTTTCTGTGTGCAATTAACCTGTGCAACCCAGGCAACCTGTCAACGCGC 7500
Db 7441 GGGCAAGCCCTTTCTGTGTGCAATTAACCTGTGCAACCCAGGCAACCTGTCAACGCGC 7500
QY 7501 CTCACCTCAGGGTAAACAGATTAACTCAACAGATGTGTCAAGTTTGTGGCAACCTGTGG 7560
Db 7501 CTCACCTCAGGGTAAACAGATTAACTCAACAGATGTGTCAAGTTTGTGGCAACCTGTGG 7560
QY 7561 TATATGGCTGAGGGGCTGCTAGGTCCCAATGCTGCGGCAAGGGCAATGAGTGCATG 7620

Db 7561 TATATGGCTGAGGGGCTGCTAGGTCCCAATGCTGCGGCAATGAGTGCATG 7620
QY 7621 CTGCCCACTGCAAGATCATCACTGTACAGATCCCTGACACCAAGAAATAGTTCGT 7680
Db 7621 CTGCCCACTGCAAGATCATCACTGTACAGATCCCTGACACCAAGAAATAGTTCGT 7680
QY 7681 CAGGTCCAGGACAGGGGCGGCAAGGTTCAAGTTTGGGCAACCACTGTCTTACCGGTCG 7740
Db 7681 CAGGTCCAGGACAGGGGCGGCAAGGTTCAAGTTTGGGCAACCACTGTCTTACCGGTCG 7740
QY 7741 AACCAAGGCTTCTACCTCTGTGGGCAACCCAGTCTCAGCTGCAAGGAGATGGCAATGG 7800
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QY 7801 GACCGTCCCCGCCCCCAAGTGTCTTGTGTGTCTGTGGGCAATCCGGGCTCCCCGCTCAC 7860
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Db 8581 GGTGTGGGTCTGACTTCAATGTGGGCTCAAGTGTGACTTATGCTGCTGGAAGGGGTAC 8640
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Db	8641	CAGCTCTCCCTGCCCCGCGTGTTCACCTGTGAGGAAATGGGTCTTGGACCGGAGACTG	8700
Qy	8701	CCTCAGTGTTCCTCTGTGTCTCGCGGGATCCTGGTGTCCCGTCCTCGTGGAGAGAG	8760
Db	8701	CCTCAGTGTTCCTCTGTGTCTCGCGGGATCCTGGTGTCCCGTCCTCGTGGAGAGAG	8760
Qy	8761	GACCGAGGCTTCTCTACAGTCACTGTCTCTTCTCTGTGCATCCCTCTGTGTGTG	8820
Db	8761	GACCGAGGCTTCTCTACAGTCACTGTCTCTTCTCTGTGCATCCCTCTGTGTGTG	8820
Qy	8821	GTGGGCTCCCAACGAGGTTTGGCAGTCAGATGGGACATGAGTGGACCCAGCCGAC	8880
Db	8821	GTGGGCTCTCCACGCGAGTTTTGGCAGTCAGATGGGACATGAGTGGACCCAGCCGAC	8880
Qy	8881	TGCATAGATCCGACCCCTGACCACTGTGCGGACCCGTGTGTGCACAGTTTGGATACG	8940
Db	8881	TGCATAGATCCGACCCCTGACCACTGTGCGGACCCGTGTGTGTGCACAGTTTGGATACG	8940
Qy	8941	AACATTTCTCAGGGTTACCAAGTTGGAAAGCACAGTCCTTCTCGTTCCAAAAGGCTAC	9000
Db	8941	AACATTTCTCAGGGTTACCAAGTTGGAAAGCACAGTCCTTCTCGTTCCAAAAGGCTAC	9000
Qy	9001	CTGCTTCAGGGTCCACACACAGGACCTGGCTCCCAACCTGACCTGGAGTGAACCCCA	9060
Db	9001	CTGCTTCAGGGTCCACACACAGGACCTGGCTCCCAACCTGACCTGGAGTGAACCCCA	9060
Qy	9061	CCTGACTGTGTCCCCACACTGACGGGACGACGAGCCGACATGCCAAGTCGTGGG	9120
Db	9061	CCTGACTGTGTCCCCACACTGACGGGACGACGAGCCGACATGCCAAGTCGTGGG	9120
Qy	9121	GCCTTGATTTGCTCCTCCATGGGGTACACGCTCATTACTCTGCCAGAGGCTTCTCC	9180
Db	9121	GCCTTGATTTGCTCCTCCATGGGGTACACGCTCATTACTCTGCCAGAGGCTTCTCC	9180
Qy	9181	TCAAGGGTGGCTCCGAGCACCGCACCTGCAGGGGGATGGGAGCTGACAGGCAAGCCG	9240
Db	9181	TCAAGGGTGGCTCCGAGCACCGCACCTGCAGGGGGATGGGAGCTGACAGGCAAGCCG	9240
Qy	9241	CCATGTGCTTGAGGTTCGGGCCCAATGGGAGACCCATCAACTGCTCCGGGAGCCACCG	9300
Db	9241	CCATGTGCTTGAGGTTCGGGCCCAATGGGAGACCCATCAACTGCTCCGGGAGCCACCG	9300
Qy	9301	TCACCCAAAGCTTGATTCCTGGGGATGTTTTGGCAAGATTCCTGTGGAAAGGGGCT	9360
Db	9301	TCACCCAAAGCTTGATTCCTGGGGATGTTTTGGCAAGATTCCTGTGGAAAGGGGCT	9360
Qy	9361	ATGATATCACGGGGAAAGACGCGACATGCTCAGAGTACGTGGCTTCCAAAGTTGCA	9420
Db	9361	ATGATATCACGGGGAAAGACGCGACATGCTCAGAGTACGTGGCTTCCAAAGTTGCA	9420
Qy	9421	ACAGCAAGTCAATCCACATGATCGACACAGTGGGGTGGAGCTGCACTTGGCTGAA	9480
Db	9421	ACAGCAAGTCAATCCACATGATCGACACAGTGGGGTGGAGCTGCACTTGGCTGAA	9480
Qy	9481	CTTACAGAAAGAAATTTTCATCTTCTACTCCAGGTGTACCAATTAACAGGGCTGTGG	9540
Db	9481	CTTACAGAAAGAAATTTTCATCTTCTACTCCAGGTGTACCAATTAACAGGGCTGTGG	9540
Qy	9541	AGATCTTATGAATAAGTTCAAGATGATCACTGGGCTTGAATGGCATGTCTGTAG	9600
Db	9541	AGATCTTATGAATAAGTTCAAGATGATCACTGGGCTTGAATGGCATGTCTGTAG	9600
Qy	9601	AGTCCCTCGGAGCCACTTCACTACAGGCTGTGTCAAGGGCCAAAGCTTTTGGGCAGT	9660
Db	9601	AGTCCCTCGGAGCCACTTCACTACAGGCTGTGTCAAGGGCCAAAGCTTTTGGGCAGT	9660
Qy	9661	TCGGCTTTCAAAGACTGACCTCAGGCTGTGAGTCAAGACCCGAGTCCATTGGCGCC	9720
Db	9661	TCGGCTTTCAAAGACTGACCTCAGGCTGTGAGTCAAGACCCGAGTCCATTGGCGCC	9720
Qy	9721	ACTTTGCTTCAAACAGCACTCAGTGGCAGCCGCGATCTGTGTGCTTTCATTCGCTTCA	9780
Db	9721	ACTTTGCTTCAAACAGCACTCAGTGGCAGCCGCGATCTGTGTGCTTTCATTCGCTTCA	9780

OY	9781	TTATTGGGGGCTTGCTGCTCTATCTCTTACAGACACAGGAAAGAACCCGAAGTCCCTTCA	9840
Db	9781	TTATTGGGGGCTTGCTGCTCTATCTCTTACAGACACAGGAAAGAACCCGAAGTCCCTTCA	9840
OY	9841	ATGCTATATGCTGGGCGCAGAGAACACCAATGTTGGGCGACATTGTGAAACCCAATGTACG	9900
Db	9841	ATGCTATATGCTGGGCGCAGAGAACACCAATGTTGGGCGACATTGTGAAACCCAATGTACG	9900
OY	9901	ACCGCAACATTCACGACCCCAACAGACATCATGGCCAGCGGCGAGTTACAGTCAGCACAG	9960
Db	9901	ACCGCAACATTCACGACCCCAACAGACATCATGGCCAGCGGCGAGTTACAGTCAGCACAG	9960
OY	9961	TGTGCACAGCAGTATATACCAACCCGGGCGCTTTTGTTCAGGTTGAACTGTA	1002
Db	9961	TGTGCACAGCAGTATATACCAACCCGGGCGCTTTTGTTCAGGTTGAACTGTA	1002
OY	10021	CCACGAGCGCGCGAGGCTGACCTGTACTGTGTCATCTCAGCTCAGTCAACCTCCCTGC	1008
Db	10021	CCACGAGCGCGCGAGGCTGACCTGTACTGTGTCATCTCAGCTCAGTCAACCTCCCTGC	1008
OY	10081	CTGATTCCTCCCTGCTCAGCCTGCGGATGCTGCGATTGCAAGGCGGCACCGCCAC	10136
Db	10081	CTGATTCCTCCCTGCTCAGCCTGCGGATGCTGCGATTGCAAGGCGGCACCGCCAC	10136
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ID	ADH71165	ADH71165 standard; DNA; 10136 BP.	
AC	ADH71165;		
XX			
DT	25-MAR-2004	(first entry)	
XX			
DE		Human gene of the invention NOV4p SEQ ID NO:61.	
XX			
XX		ds; gene; human; cytosolic; immunomodulator; neuroprotective; nootropic;	
KW		anorectic; antididiabetic; antimicrobial; antilipemic; gene therapy;	
KW		vaccini; cancer; cachexia; Alzheimer's disease; Parkinson's disease;	
KW		obesity; diabetes; infectious disease; metabolic syndrome X;	
XX		dyslipidaemia.	
OS		Homo sapiens.	
XX			
PN		WO2003102155-A2.	
PD			
XX		11-DEC-2003.	
PF			
XX		03-JUN-2003; 2003WO-US017430.	
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PR	03-JUN-2002;	2002US-0385120P.	
PR	04-JUN-2002;	2002US-0385784P.	
PR	05-JUN-2002;	2002US-0386041P.	
PR	05-JUN-2002;	2002US-0386047P.	
PR	06-JUN-2002;	2002US-0386376P.	
PR	06-JUN-2002;	2002US-0386453P.	
PR	06-JUN-2002;	2002US-0386864P.	
PR	06-JUN-2002;	2002US-0387016P.	
PR	07-JUN-2002;	2002US-0386796P.	
PR	07-JUN-2002;	2002US-0386816P.	
PR	07-JUN-2002;	2002US-0386931P.	
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PR	07-JUN-2002;	2002US-0387262P.	
PR	08-JUN-2002;	2002US-0296960P.	
PR	10-JUN-2002;	2002US-0387400P.	
PR	10-JUN-2002;	2002US-0387535P.	
PR	11-JUN-2002;	2002US-0387610P.	
PR	11-JUN-2002;	2002US-0387625P.	
PR	11-JUN-2002;	2002US-0387634P.	
PR	11-JUN-2002;	2002US-0387656P.	
PR	11-JUN-2002;	2002US-0387696P.	
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Db 6240 TTTGAGAGCAACCCCGATATGATGAGTCACTGTCAACCAATGAGCTTGAACAGC 6240
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Db 6241 TCCACAGGCGTGAATCCGAGCAGAGTACCTGGAGATATCCCGATTCAGACCTGC 6300
Qy 6301 TCTTGGCTGTGAGAGTGAAGCCGAGTAACTTCACTTCCCTCAAGTGAATGATCTCTC 6360
Db 6301 TCTTGGCTGTGAGAGTGAAGCCGAGTAACTTCACTTCCCTCAAGTGAATGATCTCTC 6360
Qy 6361 AGCAGAAACAAATATGATGATTTGATGATTTGATGATGATGATGATGATGATGAT 6420
Db 6361 AGCAGAAACAAATATGATGATTTGATGATTTGATGATGATGATGATGATGATGAT 6420
Qy 6421 CTGAAAGCCCTCAATGAGGAATTAATCAAGTCCCTGATTTGATGATGATGATGATGAT 6480
Db 6421 CTGAAAGCCCTCAATGAGGAATTAATCAAGTCCCTGATTTGATGATGATGATGATGAT 6480
Qy 6481 GTGTACCTGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6540
Db 6481 GTGTACCTGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6540
Qy 6541 TCAAGCTTATCTGAGCTGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 6600
Db 6541 TCAAGCTTATCTGAGCTGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 6600
Qy 6601 AGCAGCCAGCCCGGGGCTGATCCATCTTGGCTGCAACCGGGCTACCGCTGAGGGA 6660
Db 6601 AGCAGCCAGCCCGGGGCTGATCCATCTTGGCTGCAACCGGGCTACCGCTGAGGGA 6660
Qy 6661 CACAGATGAGCATCTGATCCGAGCAACCCCGAGGCTACCACTGTGAGGGAAGCAATC 6720
Db 6661 CACAGATGAGCATCTGATCCGAGCAACCCCGAGGCTACCACTGTGAGGGAAGCAATC 6720
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Db 6721 CCTCTGTCAAGCTCTTCTCTGTGGCTTCTGAGGCTTCTGAGGCTTCTGAGGCTTCT 6780
Qy 6781 GGCAGAGATCACAGTGGGGAACCAAGGCTGTACAGCTGAGTGAAGGCTACACCTC 6840
Db 6781 GGCAGAGATCACAGTGGGGAACCAAGGCTGTACAGCTGAGTGAAGGCTACACCTC 6840
Qy 6841 CAGGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 6900
Db 6841 CAGGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 6900
Qy 6901 GTCCACCAAGTGTGTCTGTGATCTTGTGATCTTGTGATCTTGTGATCTTGTGATCT 6960
Db 6901 GTCCACCAAGTGTGTCTGTGATCTTGTGATCTTGTGATCTTGTGATCTTGTGATCT 6960
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Db 6961 GAGCGATGAGGCTTATCTTGAAGACAGATGATGATGATGATGATGATGATGATGAT 7020
Qy 7021 TGTGACCTGTGCTATCTATATGAGCCAAAGGTCATCGCTGTGAGGCAATGAGCAA 7080
Db 7021 TGTGACCTGTGCTATCTATATGAGCCAAAGGTCATCGCTGTGAGGCAATGAGCAA 7080
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Db 7081 TGAAGCTTGGGAGCTGAGCCCACTGCGGAATCAATCTTGTGAGGAGTCTCCGAT 7140
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Db 7141 CCCCCCAATGAGCAACCGCATGGAACACTGTCTGTCTGAGGAGCAAGCATCTTCTC 7200
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7321 AACGACATCAATGGGGAGAACTACAGCTACCGGGGAGTGGTGAACCAATGCAT 7380
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7801 GACCGTCCCGCGCCCAAGTGTCTTTGGTGTCTGTGGCCATCCGGCTTCCCGCTCAC 7860
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7861 TCCCGAGTGTGAGGAGACAGTTAATCTGTGGAGAGTGGTGGATGACAGCTGACCGG 7920
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7981 TCCCTCTCTCATCTGCTCAGGAACCAAGCTGTGGAGTTTGGGTGACCTTGGGATCCG 8040
7981 TCCCTCTCTCATCTGCTCAGGAACCAAGCTGTGGAGTTTGGGTGACCTTGGGATCCG 8040
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8041 CATGGCATCCGTTTGGGGGACAGCTTGTATCCAGGACATGTATGCGCTTCACTGTGA 8100
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8161 GGTGTGAGCTGTGAGTGTGAGTGTCTTGTGGAGACCTTGGGACTCCAAGTAATGCC 8220
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8221 CGAGTGTGTTCAGTATGAGCTGTGTCTTCAAGCTTATCGTCTATAGTGTCCGGGAA 8280
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8281 GGAATACAGCCAGGCTGTCAAGCGCTGATGCTGTGATGATGATGATGATGATGATG 8340
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8521 ACCAAGCCCGTGTGCAAACTCTCATGTGTCAAGCCACTTCCGCTCATTCCCAATGGGAG 8580
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9181 TCAAGGCTGTCCGAGCAACCGCACTGTGCAAGGCTGAGCTGAGCAAGCAAGCCG 9240
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DB 9481 CTTACAAAGAAAGATTTTCATCTCTCACTCCAGGTGACAGATTACAGGCGCTGTGG 9540
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DB 9721 ACTTTGCTTCCAAAGCACTCAGTGGGAGCCGCGCATCTGTGCTTTCAATCGCCCTCA 9780
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DB 9781 TTATTGCGGGCTTGTGCTCTATCTCTACAGCACAGAGAGACCAAGTTCCTTTCA 9840
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DB 9841 ATGGCTATGCTGGCCACAGAAACCAATGTTGGGCCCATTTGAGAACCCAAATGTACG 9900
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DB 9901 ACCGCAATCCAGCCACAGACATCATGCGCAGGAGGCGGAGTTCACATGACACACAG 9960
QY 9961 TGTGCAACAGAGTATAGCCACCCGCGCTGTGCTTTTCTAGGTTGAACGTGTAAT 10020
DB 9961 TGTGCAACAGAGTATAGCCACCCGCGCTGTGCTTTTCTAGGTTGAACGTGTAAT 10020
QY 10021 CCAGAGCGCGCCGAAGCTGATCTGTAAGTCTGCTCACTGACCTGCACTCCCTGC 10080
DB 10021 CCAGAGCGCGCCGAAGCTGATCTGTAAGTCTGCTCACTGACCTGCACTCCCTGC 10080
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DB 10081 CTGATTTCCCTGCTCCAGGCTGCGAGTGCCTGCAATTCAGGCGGCGGCGCCAC 10136

RESULT 4
ADH71167
ID ADH71167 standard; DNA; 10136 BP.
XX
AC ADH71167;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human gene of the invention NOV4g SEQ ID NO:63.
XX
KM ds; gene; human; cytosolic; immunomodulator; neuroprotective; nootropic;
KM anorectic; antidiabetic; antimicrobial; antihypertensive; gene therapy;
KM vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KM obesity; diabetes; infectious disease; metabolic syndrome X;
KM dyslipidaemia.
XX
OS Homo sapiens.
XX
PN WO2003102155-A2.
XX
PD 11-DEC-2003.
XX
PF 03-JUN-2003; 2003WO-US017430.
XX
PR 03-JUN-2002; 2002US-0385120P.
PR 04-JUN-2002; 2002US-0385784P.
PR 05-JUN-2002; 2002US-0386041P.
PR 05-JUN-2002; 2002US-0386047P.
PR 06-JUN-2002; 2002US-0386376P.

PR 06-JUN-2002; 2002US-0386453P.
PR 06-JUN-2002; 2002US-0386864P.
PR 06-JUN-2002; 2002US-0387016P.
PR 07-JUN-2002; 2002US-0386796P.
PR 07-JUN-2002; 2002US-0386816P.
PR 07-JUN-2002; 2002US-0386931P.
PR 07-JUN-2002; 2002US-0386942P.
PR 07-JUN-2002; 2002US-0386971P.
PR 07-JUN-2002; 2002US-0387263P.
PR 08-JUN-2002; 2002US-0387666P.
PR 10-JUN-2002; 2002US-0387700P.
PR 10-JUN-2002; 2002US-0387535P.
PR 11-JUN-2002; 2002US-0387610P.
PR 11-JUN-2002; 2002US-0387625P.
PR 11-JUN-2002; 2002US-0387634P.
PR 11-JUN-2002; 2002US-0387666P.
PR 11-JUN-2002; 2002US-0387696P.
PR 11-JUN-2002; 2002US-0387702P.
PR 11-JUN-2002; 2002US-0387836P.
PR 11-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387933P.
PR 12-JUN-2002; 2002US-0387934P.
PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.
PR 13-JUN-2002; 2002US-0389118P.
PR 13-JUN-2002; 2002US-0389123P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389146P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389729P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389884P.
PR 19-JUN-2002; 2002US-0390006P.
PR 19-JUN-2002; 2002US-0390209P.
PR 21-JUN-2002; 2002US-0390763P.
PR 17-JUL-2002; 2002US-0396706P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402156P.
PR 09-AUG-2002; 2002US-0402256P.
PR 09-AUG-2002; 2002US-0402389P.
PR 12-AUG-2002; 2002US-0402786P.
PR 12-AUG-2002; 2002US-0402816P.
PR 12-AUG-2002; 2002US-0402821P.
PR 12-AUG-2002; 2002US-0402832P.
PR 13-AUG-2002; 2002US-0403448P.
PR 13-AUG-2002; 2002US-0403459P.
PR 13-AUG-2002; 2002US-0403531P.
PR 13-AUG-2002; 2002US-0403532P.
PR 13-AUG-2002; 2002US-0403563P.
PR 13-AUG-2002; 2002US-0403617P.
PR 15-AUG-2002; 2002US-0403617P.
PR 26-AUG-2002; 2002US-0406182P.
PR 26-AUG-2002; 2002US-0406355P.
PR 27-AUG-2002; 2002US-0406240P.
PR 12-SEP-2002; 2002US-0410084P.
PR 20-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417186P.
PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-0423798P.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.

(CURA-) CURAGEN CORP.

XX Alsobrook JP, Alvarez E, Anderson DM, Boldog FL, Casman SJ,
 PI Cateron E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellemann K,
 PI Ettenberg S, Gangoli EA, Gerlach VL, Gorman L, Gunther E, Guo X,
 PI Gusev V, Herrmann JL, Ji W, Kekuda R, Li X, Liu X, Macdonald JR,
 PI MacLachlan T, Malayankar UM, Meziel AJ, Mallet I, Misha VS,
 PI Padigaru M, Paturajan M, Pena CB, Peyman JA, Rahn D, Rastelli L,
 PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shinkens RA,
 PI Smithson C, Spytek KA, Stone DJ, Vernet CM, Voss EZ, Zhong M,
 PI Zhong H;
 XX WPI; 2004-081935/08.
 DR P-PSDB; ADH71168.
 XX New NOX polypeptides and nucleic acid molecules useful for preventing or
 PT treating NOX-associated disorders, e.g. cancer, diabetes, infection or
 PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
 XX
 PS Example 4; SEQ ID NO 63; 1880bp; English.
 CC The invention relates to a novel isolated polypeptide (NOX). A
 CC polypeptide of the invention has cytostatic, immunomodulator,
 CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
 CC antihypertensive activity, and may have a use in gene therapy, and as a
 CC vaccine. The polypeptides are encoded by NOX polynucleotides comprising
 CC any of the 303 fully defined nucleotide sequences given in the
 CC specification. The polypeptide is useful in the manufacture of a
 CC medicament for treating a syndrome associated with a human disease. The
 CC polypeptide, polynucleotide and antibody are useful in diagnosing,
 CC treating or preventing NOX-associated disorders, e.g. cancer, cachexia,
 CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
 CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
 CC further used as hybridisation probes, in chromosome mapping, tissue
 CC typing, preventive medicine, and pharmacogenomics. The present sequence
 CC encodes a NOX polypeptide of the invention.
 XX
 XX Sequence 10136 BP; 2146 A; 3059 C; 2746 G; 2185 T; 0 U; 0 Other;
 Query Match 100.0%; Score 10132.8; DB 12; Length 10136;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 10134; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCGGGGCGCCCTCCCGCGCTTGCTGCTGCTTGGAGTTTATCTCAGACTGCTG 60
 DB 1 ATGGCGGGGCGCCCTCCCGCGCTTGCTGCTGCTTGGAGTTTATCTCAGACTGCTG 60
 QY 61 GCTAGCAATCAGGACACTCTCGTGGGCTAGGACCTCTCGAGTACTCAAGACAAATT 120
 DB 61 GCTAGCAATCAGGACACTCTCGTGGGCTAGGACCTCTCGAGTACTCAAGACAAATT 120
 QY 121 GAGTTGAAGTCTCAGAGTGTGAAGCTGATGCCAGAAAGACCAAGCAAGAGCTT 180
 DB 121 GAGTTGAAGTCTCAGAGTGTGAAGCTGATGCCAGAAAGACCAAGCAAGAGCTT 180
 QY 181 GGTTAACCTCAGGTTGTGTGTCCCAAGACATTAATATGTCACAACTGGCATACCC 240
 DB 181 GGTTAACCTCAGGTTGTGTGTGTCCCAAGACATTAATATGTCACAACTGGCATACCC 240
 QY 241 GAAAGGGGCAAAAGACTAGGCTCGATTTCAGTTTGAATCCAGCTCCAGTTCACTGC 300
 DB 241 GAAAGGGGCAAAAGACTAGGCTCGATTTCAGTTTGAATCCAGCTCCAGTTCACTGC 300
 QY 301 AAGGAGGCTATGACTGCAAGGGTCCAAAGCGGATCACTGTATGAAGAGCGACATG 360
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 QY 361 TTTGGGGCTGGAGGACCAAGAGGCGAGTCTGCGAGCCCGGATGTGTATGCCACTT 420
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 QY 421 CGAGGCGCTCTGGGATCATCACTTCCCAATTTTCCCATTCAGTATGCAACATGCA 480
 DB 421 CGAGGCGCTCTGGGATCATCACTTCCCAATTTTCCCATTCAGTATGCAACATGCA 480

QY 481 CACTGNGTGTGATCATCAGACACTCAACCCCTCCAGGTGATCAAGCTCGCTTTGAG 540
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 QY 541 GAGTTTGAATTTGAGAGGGGCTATGACACCTTGACGGTGTGATGTGTGTCAGAGTGG 600
 DB 541 GAGTTTGAATTTGAGAGGGGCTATGACACCTTGACGGTGTGATGTGTGTCAGAGTGG 600
 QY 601 GACCAAGAACAGTTTCTTCACTATGTCTCAAAATGCTGTGATGACAGCCCTCAACCCA 660
 DB 601 GACCAAGAACAGTTTCTTCACTATGTCTCAAAATGCTGTGATGACAGCCCTCAACCCA 660
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 DB 661 GGGTCTCGCATCCGAGAGGACATGTCTGGGGACATCTGGAGGCGAAATGACTACTT 720
 QY 721 GAGATCTGTCTGATTAAGCAGTTTCAAGTGCAGATGCAAGGTCAAGTTCAAGTGAAGTCTCCA 780
 DB 721 GAGATCTGTCTGATTAAGCAGTTTCAAGTGCAGATGCAAGGTCAAGTGAAGTCTCCA 780
 QY 781 AAGACTTCTAATGCTGTGGAATTTGTTGCTCTGGGACAGAGATGAGCAGGCACTTGC 840
 DB 781 AAGACTTCTAATGCTGTGGAATTTGTTGCTCTGGGACAGAGATGAGCAGGCACTTGC 840
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 DB 841 GGTGACCCCTGGGATACCTGCATATAGCCGAGGAGAAAGCTCCCGGTTTACCAAGGTGAC 900
 QY 901 ACACCTCAAGTTTGAAGTGCAGGCGGCTTTGAGCTGTGTGGGACAGAGGCAATCAATGC 960
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 Db 8701 CCTCAATGTTCCTGTGTCTGTGCGGGGATCTGTGTGTCTCCGTGGGAGGAGAG 8760
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 Db 8821 GTGGGCTTCTCAAGGATTTTTCAGTCAATGAGGATGAGAGTGAAGCCAGCCAGC 8880
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 Db 8881 TGTATGATTCGACCTGTGACCAAGTGTGGGACCTGTGTGTGCAAGTTTGGGATACAG 8940
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 Db 8941 AACAAATTCAGAGGCTTCAAGGATTTGAGAGCAAGTCTCTTCCGTTGTCAAAAAGGCTAC 9000
 Qy 9001 CTGCTTCAAGGCTTCAAGGATTTGAGAGCAAGTCTCTTCCGTTGTCAAAAAGGCTAC 9060
 Db 9001 CTGCTTCAAGGCTTCAAGGATTTGAGAGCAAGTCTCTTCCGTTGTCAAAAAGGCTAC 9060
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 Db 9061 CCTGATCTGTCTCCCAAGCACTGCAAGGACGAGAGCGCAACGATGCAACGTCGAG 9120
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 Db 9121 GCCCTGATTTGCTCTTCAAGGATTTGAGAGCAAGTCTCTTCCGTTGTCAAAAAGGCTAC 9180
 Qy 9181 TCAGAGGTGCTCCGAGCAACCGCACTGCAAGGCGGATGAGACTGGAACGAGGACCCGC 9240
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Qy 9241 CCATCTGCTGAGAGTCCGCGCCAGTGGGAGAGCCCATCAACACTGCGCGGAGCCACCGC 9300
 Db 9241 CCATCTGCTGAGAGTCCGCGCCAGTGGGAGAGCCCATCAACACTGCGCGGAGCCACCGC 9300
 Qy 9301 TCACCCAGACCTTGATTCCTGGGAGATGTTTTTCCCAAGATTCCTGTGGAAGGGGCTT 9360
 Db 9301 TCACCCAGACCTTGATTCCTGGGAGATGTTTTTCCCAAGATTCCTGTGGAAGGGGCTT 9360
 Qy 9361 ATGAATACAGGGGAGAGAGCAAGCCAGATGCTAGAGTGTGCTGCTTCCAAATTGCCA 9420
 Db 9361 ATGAATACAGGGGAGAGAGCAAGCCAGATGCTAGAGTGTGCTGCTTCCAAATTGCCA 9420
 Qy 9421 ACAGAGGATCAATGCAACATGATGAGACCAAGTGGCGGTGAGAGCTGCACTGGCTGGA 9480
 Db 9421 ACAGAGGATCAATGCAACATGATGAGACCAAGTGGCGGTGAGAGCTGCACTGGCTGGA 9480
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 Db 9601 AGTCTCCGAGAGCACTTCACTCAAGGCTGTGCAAGGCTTGGGAGCTTGGGAGCT 9660
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 Db 9781 TTAATGCGGGCTTCTGCT 9840
 Qy 9841 ATGAGTATGCTGGCCAGAGAACCAACCAATGTTGAGGAGCAATTTGAGAACCCATATGAGC 9900
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 Db 10021 CCAGCAGCGGCGGAGAGTGAAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 10080
 Qy 10081 CTGATTTCCCTGTCTGAGGCTGTGCGAGTGTGCGAGTTGCGAGGCGGAGCCGCGCAC 10136
 Db 10081 CTGATTTCCCTGTCTGAGGCTGTGCGAGTGTGCGAGTTGCGAGGCGGAGCCGCGCAC 10136

RESULT 5
 ADH71141
 ID ADH71141 standard; DNA; 9951 BP.
 XX
 AC ADH71141;
 XX
 DT 25-MAR-2004 (first entry)
 XX
 DE Human gene of the invention NOV4d SEQ ID NO:37.
 XX
 KM de; gene; human; cytosolic; immunomodulator; neuroprotective; neotropic;

Db 181 GTTTAACTCAGGTGGTGTGTCTCCAAAGACATTAATGTGTCCAGACCTGGCATACCC 240
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Db 241 GAAAGGGGCAAAAGACTAGGCTCGAATTTTCAGTTAGGATCCAGGCTCAGATTCACTTCG 300
Qy 301 AACGAGGGCTATGACCTGCAAGGGGTCCAAAGCGGATCACTGTATGAAAGTGAGCGCATG 360
Db 301 AACGAGGGCTATGACCTGCAAGGGGTCCAAAGCGGATCACTGTATGAAAGTGAGCGCATG 360
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Db 361 TTTGGCGGCTGAGCGCACCAAGGCCAGTCTGGCGAGCCCGCATGTGTATGCCACCTT 420
Qy 421 CGAGGCCCCCTGGGGCATCTACCTCCCCCAATTTCCCATTCAGTATGACAACTATGCA 480
Db 421 CGAGGCCCCCTGGGGCATCTACCTCCCCCAATTTCCCATTCAGTATGACAACTATGCA 480
Qy 481 CACTGTGTGTGATCATCAGACACTCAACCCCTCCAAAGGTGATCAAGCTCGCTTTGAG 540
Db 481 CACTGTGTGTGATCATCAGACACTCAACCCCTCCAAAGGTGATCAAGCTCGCTTTGAG 540
Qy 541 GAGTTTGAATTTGAGAGGGGCTATGACACCTGACCGTCTGATGTGTGTAGATGGG 600
Db 541 GAGTTTGAATTTGAGAGGGGCTATGACACCTGACCGTCTGATGTGTGTAGATGGG 600
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Db 601 GACCGAAGACAGTTTCTTCAATGTCTCAAAATGCTGACATGACAGCCCTCAACCCCA 660
Qy 661 GGCTCTGGATCCCAAGAGCATGTCTGGGGACATGTGAGAGGAGAAATGAGCTGATCT 720
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Qy 721 GAGATCTGTCTGACATTAAGCAGTTTCAGATGCAAGGTTCAGTTTCACTGAGAGAACTTCCA 780
Db 721 GAGATCTGTCTGACATTAAGCAGTTTCAGATGCAAGGTTCAGTTTCACTGAGAGAACTTCCA 780
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Db 781 AAGACTTCTAATGTCTGTGGAATTGTGTCTCTGGGACAGAGATTCAGAGGGCAGTTTCC 840
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Db 841 GGTGACCCCTGGGATACCTGATATGAGCGGAGGGAAGGCTCCCGTTTCAACACCGGTGAC 900
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Db 1501 AACAGCGCTGTCTGGGTGTAAGTCCCTGTGTGTGTGCTGACCTGCTTGGCCAGCGGC 1560
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Db 1741 TACCAAGGAGCCAGGTTCCCGAGTTCTCATCAGACACAGGACATACCTTACCTCTCTC 1800
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Db 1801 TTCTCTACCGAAGAGTCACTGGACATCGGCTTTCAGCTCTCGCTATGAGACTATACA 1860
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Db 1861 CTGAGTGCAGACACTGTCTGATCCAGGAATCCAGTAATGAGACGGGTATGAGGAAT 1920
Qy 1921 GACTTCTAGTGGGCGCGTGTGACCTTCACTGAGCTCGGGCTCAATTAATGATGAC 1980
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Db 2281 ATCAGGCTGGGCTGTAGGCAATTAATGAGTGTGAGGCTGCTTCACTGATTTCTCC 2340
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QY 4561 AACTCGGCTATGCGCTTCAAGAGGCTGCGCAGAGATGAGTGTGCTTGTGCGGACC 4620

D	4561	AACTCCGGCTATGCTCTCAGGGGTCGCCAGATCAGTGCCTCCCTGTGCTGGGCC	4620
Q	4621	TTGGCCCAATGGATGTCTCAGCGCCACGTGTGTGTCGGCTGTGAGGCACTCA	4680
D	4621	TTGGCCCAATGGATGTCTCAGCGCCACGTGTGTGTCGGCTGTGAGGCACTCA	4680
Q	4661	GAGCCCAAGGGGCACTCTGTCTCCCTGGCTTCCAGAGCCGTACTCAAGCTCAAC	4740
D	4661	GAGCCCAAGGGGCACTCTGTCTCCCTGGCTTCCAGAGCCGTACTCAAGCTCAAC	4740
Q	4741	TGTGTGTGAAGATGTGTGTCCCGAAGGCGTGGCATTCAGATCCAAAGTTGTAGTTT	4800
D	4741	TGTGTGTGAAGATGTGTGTCCCGAAGGCGTGGCATTCAGATCCAAAGTTGTAGTTT	4800
Q	4801	GTGACAGAGCAGAACTGGGACTCGCTGGAAATTTGATGTGTGACATTAACATCTAAAC	4860
D	4801	GTGACAGAGCAGAACTGGGACTCGCTGGAAATTTGATGTGTGACATTAACATCTAAAC	4860
Q	4861	ATGCTGGGAGATTTCTCAGAAACAACCGTGCCTGCCTTTCTGAACAGACCTCCACAG	4920
D	4861	ATGCTGGGAGATTTCTCAGAAACAACCGTGCCTGCCTTTCTGAACAGACCTCCACAG	4920
Q	4921	CTCTACCTTCATTTCTACAGATTCACGCGATCTGAGCGTCTTCACTTGAAGTAC	4980
D	4921	CTCTACCTTCATTTCTACAGATTCACGCGATCTGAGCGTCTTCACTTGAAGTAC	4980
Q	4981	AAAACGGTGGGCTCAGACAGTTGTCGGAACCTGCTGTGCCAGATTAACGGGGTGAAGCT	5040
D	4981	AAAACGGTGGGCTCAGACAGTTGTCGGAACCTGCTGTGCCAGATTAACGGGGTGAAGCT	5040
Q	5041	GGCGAGCGCTACTTGTGTGATGATGTGTGTCCTTTCAGTGTGTGAGCCGGATATGCTCTC	5100
D	5041	GGCGAGCGCTACTTGTGTGATGATGTGTGTCCTTTCAGTGTGTGAGCCGGATATGCTCTC	5100
Q	5101	CAGGGCCACGCCACATCTCTCTGCAATGCCCGGAACAAGTGCAGCGCATGGAACCTACCTCTCT	5160
D	5101	CAGGGCCACGCCACATCTCTCTGCAATGCCCGGAACAAGTGCAGCGCATGGAACCTACCTCTCT	5160
Q	5161	CCACTCTGTATTGTCACAGTGTGGGGGAACAGTGAAGAGATGGAAGGGGTATCTGTAGC	5220
D	5161	CCACTCTGTATTGTCACAGTGTGGGGGAACAGTGAAGAGATGGAAGGGGTATCTGTAGC	5220
Q	5221	CCGGGCTTCCAGGCACTACCCCAAGTAACTGACTGCTCTCTGGAAAAATGACTGCGCC	5280
D	5221	CCGGGCTTCCAGGCACTACCCCAAGTAACTGACTGCTCTCTGGAAAAATGACTGCGCC	5280
Q	5281	GTGGGCTTTGAGCTCACAATCCAGTTCCTGAACTTCTCACCGAGCCCAACAGACTAC	5340
D	5281	GTGGGCTTTGAGCTCACAATCCAGTTCCTGAACTTCTCACCGAGCCCAACAGACTAC	5340
Q	5341	ATAGAAATCCCGAATGAGGCCCTATAGAACAAGCCGATGATGGGAAGTTCAAGTGAAGC	5400
D	5341	ATAGAAATCCCGAATGAGGCCCTATAGAACACAGCCGATGATGGGAAGTTCAAGTGAAGC	5400
Q	5401	GAGCTTCCAGAGCTCTCTCTCTCTCCAGCTCCACAGACCAACCGTGTATTTCCAGAGCAC	5460
D	5401	GAGCTTCCAGAGCTCTCTCTCTCTCTCCAGCTCCACAGACCAACCGTGTATTTCCAGAGCAC	5460
Q	5461	CACCTCCCAAGATCGGCCAGAGATTCAAGCTGGAGTATCAGGGCTATGAACCTTCAAGAGTGC	5520
D	5461	CACCTCCCAAGATCGGCCAGAGATTCAAGCTGGAGTATCAGGGCTATGAACCTTCAAGAGTGC	5520
Q	5521	CCAGACCCAGAGCCCTTTGGCCAAATGGCAATTGAGAGGGAGCGGTACCAAGTGGGACAA	5580
D	5521	CCAGACCCAGAGCCCTTTGGCCAAATGGCAATTGAGAGGGAGCGGTACCAAGTGGGACAA	5580
Q	5581	TCAGTGAACCTTGAAGTGCCTCCCGGGGTATCAATTGACTGTGGCAACCTGTCTCTGACGTGT	5640
D	5581	TCAGTGAACCTTGAAGTGCCTCCCGGGGTATCAATTGACTGTGGCAACCTGTCTCTGACGTGT	5640
Q	5641	CAACATGGCAACCAACCGGAATGGGACCAACCCCTGCCCAAGTGTGAAGTCCCTTGTGGC	5700

Db	5641	CAACA TGGCACCAACCGGAACTGGGAGCCACCCCTGGCCAAAGTGAAGTCCCTTGAGCC	5700
Qy	5701	GGGAA CATCACTTCTTCCACCGCACTGTGTACTCCCGGGGTTCCTAGCCGTACTCC	5760
Db	5701	GGGAA CATCACTTCTTCCACCGCACTGTGTACTCCCGGGGTTCCTAGCCGTACTCC	5760
Qy	5761	AGCTCCCAAGGACTGTGTCTGGCTGTATCAACCGGTGCCAATTGGCCAAATGGCGTCCGCTCAAC	5820
Db	5761	AGCTCCCAAGGACTGTGTCTGGCTGTATCAACCGGTGCCAATTGGCCAAATGGCGTCCGCTCAAC	5820
Qy	5821	CTCAGCCCTGTGACAGACAGACCCCTCTGGAAATTTCAATCACTCTGGGATGGGCCACAG	5880
Db	5821	CTCAGCCCTGTGACAGACAGACCCCTCTGGAAATTTCAATCACTCTGGGATGGGCCACAG	5880
Qy	5881	CAAA CAGACCA CGGCTCGGCGCTTTCACCCGAGCATGGCCAAAGAAA CAGTCAAGT	5940
Db	5881	CAAA CAGACCA CGGCTCGGCGCTTTCACCCGAGCATGGCCAAAGAAA CAGTCAAGT	5940
Qy	5941	TCATTC AACAGGTCCTGTCTCAAGTTCCACCGTATGACGCCAAGGGGGGATTTTGCC	6000
Db	5941	TCATTC AACAGGTCCTGTCTCAAGTTCCACCGTATGACGCCAAGGGGGGATTTTGCC	6000
Qy	6001	ATAGCTTCTCCGCTTATCGACTACCAAAATAGCCCTCCTCCACCATCTCCCAAGCC	6060
Db	6001	ATAGCTTCTCCGCTTATCGACTACCAAAATAGCCCTCCTCCACCATCTCCCAAGCC	6060
Qy	6061	GAAGTCGT CACAGAAATGAAGAA TTTCAATATAGTGA CATGTACGCTACAGATGCCTC	6120
Db	6061	GAAGTCGT CACAGAAATGAAGAA TTTCAATATAGTGA CATGTACGCTACAGATGCCTC	6120
Qy	6121	CTGGCTTTACCTTAGTGGGGAATGAATTTTGACCTTGCAACTTGGAACTTACCTGAC	6180
Db	6121	CTGGCTTTACCTTAGTGGGGAATGAATTTTGACCTTGCAACTTGGAACTTACCTGAC	6180
Qy	6181	TTTGAAGGACACCCCGGATATGTGAAGTGCACGTGCCAACAAATGAGCTTCTGACAGAC	6240
Db	6181	TTTGAAGGACACCCCGGATATGTGAAGTGCACGTGCCAACAAATGAGCTTCTGACAGAC	6240
Qy	6241	TCACA GGCCTGATCTTGAGCCACAGAGCTACCCCTGGAAGCTATCCCGATTCCAGACCTGC	6300
Db	6241	TCACA GGCCTGATCTTGAGCCACAGAGCTACCCCTGGAAGCTATCCCGATTCCAGACCTGC	6300
Qy	6301	TCTTGGCTGTGAGAGTGGAGCCCGACTATTA CATCTTCCTCACA GTGAGTACTTCTCTC	6360
Db	6301	TCTTGGCTGTGAGAGTGGAGCCCGACTATTA CATCTTCCTCACA GTGAGTACTTCTCTC	6360
Qy	6361	AGCGAAGAACATATGATGAGTTTGATGATTTTGAATGTGCCATAGGACAGAGTCTCTGC	6420
Db	6361	AGCGAAGAACATATGATGAGTTTGATGATTTTGAATGTGCCATAGGACAGAGTCTCTGC	6420
Qy	6421	CTGAAAGCCCTCAGTGGGAATTA CTCAAGCTCCCTGATTTGTCA CAGACTCAAGCAACTCT	6480
Db	6421	CTGAAAGCCCTCAGTGGGAATTA CTCAAGCTCCCTGATTTGTCA CAGACTCAAGCAACTCT	6480
Qy	6481	GTGTATCTGCGTGTGTCA TCTGATCA GCGCTACAA TGGAAAGGCTTCAAGATCCGCTAT	6540
Db	6481	GTGTATCTGCGTGTGTCA TCTGATCA GCGCTACAA TGGAAAGGCTTCAAGATCCGCTAT	6540
Qy	6541	TCAGCCCTTACTGCA GCGCTGCCAGGGCTCACTCCATGCTTACTTCAAGCCCAAC	6600
Db	6541	TCAGCCCTTACTGCA GCGCTGCCAGGGCTCACTCCATGCTTACTTCAAGCCCAAC	6600
Qy	6601	AGCA CCGACCGCGGGGCTTCATCACTTTGGTGAACGCGCGCTACCGCTGGTGGGA	6660
Db	6601	AGCA CCGACCGCGGGGCTTCATCACTTTGGTGAACGCGCGCTACCGCTGGTGGGA	6660
Qy	6661	CACAGCATGGCCATCTGTATCCCGGACCCCGAGGCTAACCACTGTGAGCGAAGCATC	6720
Db	6661	CACAGCATGGCCATCTGTATCCCGGACCCCGAGGCTAACCACTGTGAGCGAAGCATC	6720
Qy	6721	CCTCTCTGTCAAGCTTTTCTGTGGGCTTCTTGAGGCCCGCCCAAGATGGAATGTGTGTT	6780
Db	6721	CCTCTCTGTGTCAAGCTTTTCTGTGGGCTTCTTGAGGCCCGCCCAAGATGGAATGTGTGTT	6780
Qy	6781	AGCTCTTTCTCTGTGGGCTTCTTGAGGCCCGCCCAAGATGGAATGTGTGTT	6840
Db	6781	AGCTCTTTCTCTGTGGGCTTCTTGAGGCCCGCCCAAGATGGAATGTGTGTT	6840

6781 GGCAAGAGTACACAGTGGGAACCAAGCCGNTGACAGCTGCAGTAGGAGGCTACCACTTC 6840
6552 GGCAAGAGTACACAGTGGGAACCAAGCCATGTACAGCTGCAGTAGAAGCTACCACTTC 6651
6841 CAGGAGGCGCTGAGAGGCCATCTGCAGAGTGTCTGACACAGAGGCTTATGAGCAACCGCAAT 6900
6652 CAGGAGGCGCTGAGAGGCCATCTGCAGAGTGTCTGACACAGAGGCTTATGAGCAACCGCAAT 6711
6901 GTCCACCAACAGTGTGTCTCTGTGACTTGTCTGATGTCTGATGATGATGATGATGATGATGAT 6960
6712 GTCCACCAACAGTGTGTCTCTGTGACTTGTCTGATGTCTGATGATGATGATGATGATGATGAT 6771
6961 GGCCCATGAGAGGCTTATCTTTGAGACACAGTATCTGATCTGATCTGATCTGATCTGATCTGATCT 7020
6772 GGCCCATGAGAGGCTTATCTTTGAGACACAGTATCTGATCTGATCTGATCTGATCTGATCTGATCT 6831
7021 TGTGACCCCTGCTACTATCTACTGAGCCAAAGGCTCATCCGCTGTCAAGGCCAATGGCAAA 7080
6832 TGTGACCCCTGCTACTATCTACTGAGCCAAAGGCTCATCCGCTGTGTCAAGGCCAATGGCAAA 6891
7081 TGTGACCCCTGAGGAGCTTACGCCCACTGTGCCAATCATCTCTGTGTGAGAGCTCCGCAAT 7140
6892 TGTGACCCCTGAGGAGCTTACGCCCACTGTGCCAATCATCTCTGTGTGAGAGCTCCGCAAT 6951
7141 CCCCCCAATGGGCAACGCGACCTGAGGAAACATGTGTCTGATCTGATCTGATCTGATCTGATCTGATCT 7200
6952 CCCCCCAATGGGCAACGCGACCTGAGGAAACATGTGTCTGATCTGATCTGATCTGATCTGATCTGATCT 7011
7201 TGTGACCCCTGAGGAGCTTACGCCCACTGTGTGAGGCTTCAAGGCTGCTGATGATGATGATGATGATGAT 7260
7012 TGTGACCCCTGAGGAGCTTACGCCCACTGTGTGAGGCTTCAAGGCTGCTGATGATGATGATGATGATGAT 7071
7261 TGTGAGTGTCTGAGAGT 7320
7072 TGTGAGT 7131
7321 AACGGAACATCAATGGGGAAGAACTACAGCTACCGGGGCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 7380
7132 AACGGAACATCAATGGGGAAGAACTACAGCTACCGGGGCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 7191
7381 GCTGT 7440
7192 GCTGT 7251
7441 GGCAAGAGGCTTGT 7500
7252 GGCAAGAGGCTTGT 7307
7501 CTCACTCAGGGTAAACAGTTTAACTTCAACGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 7560
7308 CTCACTCAGGGTAAACAGTTTAACTTCAACGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 7367
7561 TATATGT 7620
7368 TATATGT 7427
7621 GTGCCCACTGCAAGATCATCACTGTACAGATCTGTGACACCAAGAAATGTGTGTGTGTGTGTGTGTGTGT 7680
7428 GTGCCCACTGCAAGATCATCACTGTACAGATCTGTGACACCAAGAAATGTGTGTGTGTGTGTGTGTGTGT 7487
7681 CAGGTTCACGCAAGGAGGCGCGGCAAGGTTCACTTCCGACACAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 7740
7488 CAGGTTCACGCAAGGAGGCGCGGCAAGGTTCACTTCCGACACAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 7547
7741 AACCAAGGCTTGT 7800
7548 AACCAAGGCTTGT 7607
7801 GACGCTCCCGCGCCCAAGT 7852
7608 GACGCTCCCGCGCCCAAGT 7667

7853 GCCTCACTCCAGAGT 7912
7668 GCCTCACTCCAGAGT 7727
7913 GCATCGGCAAGGCTTGT 7972
7728 GCATCGGCAAGGCTTGT 7787
7973 GGAAGT 8032
7788 GGAAGT 7847
8033 TCCGAGCTCATGAGCATCGTTGT 8092
7848 TCCGAGCTCATGAGCATCGTTGT 7907
8093 GCTGTGAAGCTGTGACGAGT 8152
7908 GCTGTGAAGCTGTGACGAGT 7967
8153 CGTGTGAAGCTGTGACGAGT 8212
7968 CGTGTGAAGCTGTGACGAGT 8027
8213 GTAATGCCGAGT 8272
8028 GTAATGCCGAGT 8087
8273 GCGGGGAAAGATTAAGT 8332
8088 GCGGGGAAAGATTAAGT 8147
8333 GGAAGAGAGT 8392
8148 GGAAGAGAGT 8207
8393 ATGGCTCTTGGCTGGGCAATGACTTCAAGT 8452
8208 ATGGCTCTTGGCTGGGCAATGACTTCAAGT 8267
8453 CTGCTATATGAT 8512
8268 CTGCTATATGAT 8327
8513 GGAATGGAACCAACCGGCTGTGCAAGGCTCAAGT 8572
8328 GGAATGGAACCAACCGGCTGTGCAAGGCTCAAGT 8387
8573 ATGGGAAGT 8632
8388 ATGGGAAGT 8447
8633 AGGGGTACAGCTCTCTCTGCGCGGCTGTCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 8692
8448 AGGGGTACAGCTCTCTCTGCGCGGCTGTCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 8507
8693 GAGAGCTGCTCAATGT 8752
8508 GAGAGCTGCTCAATGT 8567
8753 GGAAGAGGAGCCGAGGCTTCTCTACAGT 8812
8568 GGAAGAGGAGCCGAGGCTTCTCTACAGT 8627
8813 TGT 8872
8628 TGT 8687
8873 AGCCCAAGT 8932
8688 AGCCCAAGT 8747
8933 GGATTAAGAAACAATTTCTCAGGCTTACCAAGT 8992

Db	8748	GGATACGAACAATTTCTCAGGGCTTACCAAGTTGGAACACAGTCTCTTCCGTTGTCAAA	8807
Oy	8893	AAGGCTACCTGCTTCAGGGCTCCACACACAGACCTGCTCCCAAACCTGACTGGAGTG	9052
Db	8808	AAGGCTACCTGCTTCAGGGGCTCCACACACAGAACCTGCTCCAAACCTGACTGGAGTG	8867
Oy	9053	GAACCCCACTGACTGTGTCTCCCACTGACAGGACGCCAGAGACCCAAACGATGCCA	9112
Db	8868	GAACCCCACTGACTGTGTCTCCCACTGACAGGACGCCAGAGAGCCAAACGATGCCA	8927
Oy	9113	ACGTGCGGGGCTTGGATTTGGCCCTCAATGGGCTCAACGCTCATTTACTCTCGGACGAGGG	9172
Db	8928	ACGTGCGGGGCTTGGATTTGGCCCTCAATGGGCTCAACGCTCATTTACTCTCGGACGAGGG	8987
Oy	9173	CTTCTCCCTCAAGGGGTGCTCCAGACACCGACCTGCAAGGCGGATGAGCAGTGCACAG	9232
Db	8988	CTTCTCCCTCAAGGGGTGCTCCAGACACCGACCTGCAAGGCGGATGAGCAGTGCACAG	9047
Oy	9233	CAAGCCGCCCATCTGTGCTTGAAGGTCCGGCCAGTGGGAGACCATCAACTGCCCCGGA	9292
Db	9048	CAAGCCGCCCATCTGTGCTTGAAGGTCCGGCCAGTGGGAGACCATCAACTGCCCCGGA	9107
Oy	9293	GCCACCGCTCACCAAGCTTGATTCCTGGGGATGTTTTGGCAAGATTCCTCGTGGA	9352
Db	9108	GCCACCGCTCACCAAGCTTGATTCCTGGGGATGTTTTGGCAAGATTCCTCGTGGA	9167
Oy	9353	AGGGGCTCATTAATACAGGGGAGAGAGACAGCCAGCCATGCTCAGAGTGACTGGCTTCCA	9412
Db	9168	AGGGGCTCATTAATACAGGGGAGAGAGACAGCCAGCCATGCTCAGAGTGACTGGCTTCCA	9227
Oy	9413	AGTTGCCAACGACAAAGTCAAATGCAATGATGACACAGTGGCGGTGAGCTGCACCT	9472
Db	9228	AGTTGCCAACGACAAAGTCAAATGCAATGATGACACAGTGGCGGTGAGCTGCACCT	9287
Oy	9473	GGCTGGAACTTACAAAGAAAGAAATTTTCATCTTCCTACCTCAGAGTGAACCAAGTTACAG	9532
Db	9288	GGCTGGAACTTACAAAGAAAGAAATTTTCATCTTCCTACCTCAGAGTGAACCAAGTTACAG	9347
Oy	9533	GCCTGGAGATCTTTATGAATAAGTTCAAAAGATGATCATCTGGGCTTTAGATGGCCATGT	9592
Db	9348	GCCTGGAGATCTTTATGAATAAGTTCAAAAGATGATCATCTGGGCTTTAGATGGCCATGT	9407
Oy	9593	CTGCTCAGAGTCTTCGGAAGCCACTTTCATCTACAAAGGCTGTCAAGGCCCAAGGCTT	9652
Db	9408	CTGCTCAGAGTCTTCGGAAGCCACTTTCATCTACCAAGGCTGTCAAGGCCCAAGGCTT	9467
Oy	9653	TGGGCAAGTTCCGGCTTTCAAAGACTGGACCTCAGGCTGCTGGAGTCAAGCCCCGAATCCAT	9712
Db	9468	TGGGCAAGTTCCGGCTTTCAAAGACTGGACCTCAGGCTGCTGGAGTCAAGCCCCGAATCCAT	9527
Oy	9713	TGGGCGGCACTTGGCTTCCAAACAGCAGCTCAGTGGGACGGCGCATCCTGGTGGCTTCAAT	9772
Db	9528	TGGGCGGCACTTGGCTTCCAAACAGCAGCTCAGTGGGACGGCGCATCCTGGTGGCTTCAAT	9587
Oy	9773	CGCCCTCATTTATTCGGGCTTCTGTGCTCTATCTCTACAAACAGAGAGAACCCAAAGT	9832
Db	9588	CGCCCTCATTTATTCGGGCTTCTGTGCTCTATCTCTACAAACAGAGAGAACCCAAAGT	9647
Oy	9833	TCCTTTCAAATGGCTATGCTGGCCACGAGAACCAATGTTCCGGGCCACATTTGAGAACCC	9892
Db	9648	TCCTTTCAAATGGCTATGCTGGCCACGAGAACCAATGTTCCGGGCCACATTTGAGAACCC	9707
Oy	9893	AATGATGACGCGCAACATCCAGCCACAGACATCATATGGCCAGGAGGCGGAGTTCAAGT	9952
Db	9708	AATGATGACGCGCAACATCCAGCCACAGACATCATATGGCCAGGAGGCGGAGTTCAAGT	9767
Oy	9953	CAGCACAATGTGCACAGCAGTATAGCACCCGGGCTGGCGCTTTTTCCTAGTGTGA	10012
Db	9768	CAGCACAATGTGCACAGCAGTATAGCACCCGGGCTGGCGCTTTTTCCTAGTGTGA	9827
Oy	10013	CTGGTACTCCAGCAGCGCGGCAAGCTGATCTGCTGCCATCTCAGTCACTGCAAC	10072

Dd	9828	CTGCTATCTCAGCAGCGCCGGAAGCTGACTGACTGATCTGACCTCATCTCAGCTCAGC	9887
+			
Oy	10073	CTCCCTGCTGATTTCCTCTGCTCAGCTGCGGAGTGCCTGGATTGACGGCGCCACCG	10132
Dd	9888	CTCCCTGCTGATTCCCTGCTCAGCTGCGAGTGCCTGGATTGACGGCGCCACCG	9947
Oy	10133	CCAC 10136	
Dd	9948	CCAC 9951	
RESULT 6			
ID	ADH71135		
XX	ADH71135	standard; DNA; 10655 BP.	
AC	ADH71135;		
XX			
DT	25-MAR-2004	(first entry)	
XX			
DE	Human gene of the invention NOVA SEQ ID NO:31.		
XX			
XX	ds; gene; human; cytosolic; immunomodulator; neuroprotective; nootropic;		
XX	anorectic; antidiabetic; antimicrobial; antilipemic; gene therapy;		
KW	vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;		
KM	obesity; diabetes; infectious disease; metabolic syndrome X;		
KW	dyslipidaemia.		
XX			
OS	Homo sapiens.		
XX			
PN	WO2003102155-A2.		
XX			
PD	11-DEC-2003.		
XX			
PF	03-JUN-2003; 2003WO-US017430.		
XX			
PR	03-JUN-2002; 2002US-0385120P.		
PR	04-JUN-2002; 2002US-0385784P.		
PR	05-JUN-2002; 2002US-0386041P.		
PR	05-JUN-2002; 2002US-0386047P.		
PR	06-JUN-2002; 2002US-0386376P.		
PR	06-JUN-2002; 2002US-0386453P.		
PR	06-JUN-2002; 2002US-0386864P.		
PR	06-JUN-2002; 2002US-0387016P.		
PR	07-JUN-2002; 2002US-0387696P.		
PR	07-JUN-2002; 2002US-0386816P.		
PR	07-JUN-2002; 2002US-0386931P.		
PR	07-JUN-2002; 2002US-0386942P.		
PR	07-JUN-2002; 2002US-0386971P.		
PR	07-JUN-2002; 2002US-0387262P.		
PR	08-JUN-2002; 2002US-0296960P.		
PR	10-JUN-2002; 2002US-0387400P.		
PR	10-JUN-2002; 2002US-0387535P.		
PR	11-JUN-2002; 2002US-0387610P.		
PR	11-JUN-2002; 2002US-0387625P.		
PR	11-JUN-2002; 2002US-0387634P.		
PR	11-JUN-2002; 2002US-0387668P.		
PR	11-JUN-2002; 2002US-0387702P.		
PR	11-JUN-2002; 2002US-0387836P.		
PR	11-JUN-2002; 2002US-0387859P.		
PR	12-JUN-2002; 2002US-0387933P.		
PR	12-JUN-2002; 2002US-0387934P.		
PR	12-JUN-2002; 2002US-0387960P.		
PR	12-JUN-2002; 2002US-0388022P.		
PR	12-JUN-2002; 2002US-0388096P.		
PR	13-JUN-2002; 2002US-0389123P.		
PR	14-JUN-2002; 2002US-0389118P.		
PR	14-JUN-2002; 2002US-0389120P.		
PR	14-JUN-2002; 2002US-0389144P.		
PR	14-JUN-2002; 2002US-0389146P.		
PR	17-JUN-2002; 2002US-0389729P.		
PR	17-JUN-2002; 2002US-0389742P.		
PR	18-JUN-2002; 2002US-0389884P.		

19-JUN-2002; 2002US-0390006P.
 PR 19-JUN-2002; 2002US-0390209P.
 PR 21-JUN-2002; 2002US-0390763P.
 PR 17-JUL-2002; 2002US-0396706P.
 PR 06-AUG-2002; 2002US-0401628P.
 PR 09-AUG-2002; 2002US-0402156P.
 PR 09-AUG-2002; 2002US-040256P.
 PR 09-AUG-2002; 2002US-040289P.
 PR 12-AUG-2002; 2002US-040286P.
 PR 12-AUG-2002; 2002US-040281P.
 PR 12-AUG-2002; 2002US-040283P.
 PR 13-AUG-2002; 2002US-040348P.
 PR 13-AUG-2002; 2002US-0403459P.
 PR 13-AUG-2002; 2002US-0403531P.
 PR 13-AUG-2002; 2002US-0403532P.
 PR 13-AUG-2002; 2002US-0403563P.
 PR 13-AUG-2002; 2002US-0406317P.
 PR 15-AUG-2002; 2002US-040617P.
 PR 26-AUG-2002; 2002US-0406182P.
 PR 26-AUG-2002; 2002US-0406355P.
 PR 27-AUG-2002; 2002US-0406240P.
 PR 12-SEP-2002; 2002US-0410084P.
 PR 20-SEP-2002; 2002US-0412528P.
 PR 23-SEP-2002; 2002US-0412731P.
 PR 30-SEP-2002; 2002US-0414801P.
 PR 30-SEP-2002; 2002US-0414839P.
 PR 30-SEP-2002; 2002US-0414840P.
 PR 30-SEP-2002; 2002US-0414954P.
 PR 09-OCT-2002; 2002US-0417186P.
 PR 09-OCT-2002; 2002US-0417406P.
 PR 23-OCT-2002; 2002US-0420639P.
 PR 28-OCT-2002; 2002US-0421156P.
 PR 31-OCT-2002; 2002US-0422690P.
 PR 01-NOV-2002; 2002US-0423130P.
 PR 05-NOV-2002; 2002US-0423798P.
 PR 05-NOV-2002; 2002US-0423798P.
 PR 12-NOV-2002; 2002US-0425453P.
 XX
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Alsbrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
 PI Catereron E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
 PI Etlberg S, Gangoli E, Gerlach VL, Gorman L, Gunther E, Guo X;
 PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, MacDougall JR;
 PI MacLachlan T, Malvankar UM, Mezick AJ, Miller I, Mishra VS;
 PI Padigan M, Paturajan M, Pena CE, Peyman JA, Raha D, Rastelli L;
 PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shinkels RA;
 PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
 PI Zhong H;
 XX
 DR WPI: 2004-081935/08.
 DR P-Psdb; ADH71136.
 XX
 PT New NOXV polypeptides and nucleic acid molecules useful for preventing or
 PT treating NOXV-associated disorders, e.g. cancer, diabetes, infection or
 PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
 XX
 PS Example 4; SEQ ID NO 31; 1880bp; English.

XX
 CC The invention relates to a novel isolated polypeptide (NOXV). A
 CC polypeptide of the invention has cytostatic, immunomodulator,
 CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
 CC antihypertensive activity, and may have a use in gene therapy, and as a
 CC vaccine. The polypeptides are encoded by NOXV polynucleotides comprising
 CC any of the 303 fully defined nucleotide sequences given in the
 CC specification. The polypeptide is useful in the manufacture of a
 CC medicament for treating a syndrome associated with a human disease. The
 CC polypeptide, polynucleotide and antibody are useful in diagnosing,
 CC treating or preventing NOXV-associated disorders, e.g. cancer, cachexia,
 CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
 CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
 CC further used as hybridisation probes, in chromosome mapping, tissue

CC typing, preventive medicine, and pharmacogenomics. The present sequence
 CC encodes a NOXV polypeptide of the invention.

XX Sequence 10655 BP; 2255 A; 3236 C; 2879 G; 2285 T; 0 U; 0 Other;

Query Match 93.8%; Score 9508; DB 12; Length 10655;

Best Local Similarity 98.0%; Pred. No. 0;
 Matches 9702; Conservative 0; Mismatches 105; Indels 91; Gaps 4;

QY 101 AGCTAGTGAAGAACCAATTGAGTTGAAGTCTGAGGTGTGAAGTGTGCTCCAGCAAG 160
 DB 842 ACCAAGTCAAGAACCAATTGAGTTGAAGTCTGAGGTGTGAAGTGTGCTCCAGCAAG 901
 QY 161 ACAACAGCCAGAACAGCTGTGTTAACTCAGTTGGTGTGCCAAGACATAATATGT 220
 DB 902 ACAACAGCCAGAACAGCTGTGTTAACTCAGTTGGTGTGCCAAGACATAATATGT 961
 QY 221 GTCCAGACCTGGGATACCCGAAAGGGCAAAAGACTAGGCTCGATTTCAGTTAGAT 280
 DB 962 GTCCAGACCTGGGATACCCGAAAGGGCAAAAGACTAGGCTCGATTTCAGTTAGAT 1021
 QY 281 CCAGGTCCTCACTTCACTGCAAGAGGCTATGACCTGCAAGGTTCCAGGCGATCACT 340
 DB 1022 CCAGGTCCTCACTTCACTGCAAGAGGCTATGACCTGCAAGGTTCCAGGCGATCACT 1081
 QY 341 GTATGAAGAGGAGCAATGTTTGGGCTGGAGCCAGCAAGGCGATGCGAGGCC 400
 DB 1082 GTATGAAGAGGAGCAATGTTTGGGCTGGAGCCAGCAAGGCGATGCGAGGCC 1141
 QY 401 GCATGTGTGATGCCACCTTGGAGGCCCTCTGGGCAATCATCACTCCCAATTTCCCA 460
 DB 1142 GCATGTGTGATGCCACCTTGGAGGCCCTCTGGGCAATCATCACTCCCAATTTCCCA 1201
 QY 461 TTCAGTATGACAAGACACATGTGTGTGATGATCAACGACTCAACCTCCCAAG 520
 DB 1202 TTCAGTATGACAAGACACATGTGTGTGATGATCAACGACTCAACCTCCCAAG 1261
 QY 521 TGATCAAGCTGCGCTTTGAGGAGTTTATTTGAGAGGGGCTATGACACCTGACGCTG 580
 DB 1262 TATATCAAGCTGCGCTTTGAGGAGTTTATTTGAGAGGGGCTATGACACCTGACGCTG 1321
 QY 581 GTGATGTGTGATGAGAGTGGGAGCCAGAAAGACATTTCTTACATGTTCCAAATGCTGCA 640
 DB 1322 GTGATGTGTGATGAGAGTGGGAGCCAGAAAGACATTTCTTACATGTTCCAAATGCTGCA 1365
 QY 641 GTGACAGCCCTCACACCCAGGCTCTGCAATCCAGAGAGATGTGGGACATCTGGA 700
 DB 1366 ----- 1365
 QY 701 GGCAGAAATGAGACTGTACTTGAATCTGTCTGTGACATTAGCAGTTCAAGATCAAGTTCAG 760
 DB 1366 -----CTGACAGATACATCGGTCCCGATCTCATTTGTAGACACCAATCATCAATAGT 1417
 QY 761 GTTAGTGAAGAGTCTCCAAAGACTTCTTAATGCTGTGGAACCTGTGCTCTGGAGCAG 820
 DB 1418 GGTCTCTCTTCCACATGATGAGGAGTGGAGTCTCTGGGATTTCAAGGCTTTTATGAG 1477
 QY 821 AGATGAGAGGAGGAGTGTGGGTGTAACCTGGCAATACCTGCAATATAGGCGGAGGAGGCT 880
 DB 1478 AGATGAGAGGAGGAGTGTGGGTGTAACCTGGCAATACCTGCAATATAGGCGGAGGAGGCT 1537
 QY 881 CCCGGTTTCAACAGGTCACACTCACTCAAGTTTGAAGTCCAGCCGCTTTAGAGTGTGG 940
 DB 1538 CCCGGTTTCCGACAGGTCACACTCACTCAAGTTTGAAGTCCAGCCGCTTTAGAGTGTGG 1597
 QY 941 GACAGAAAGGCAATACATGCAATGCAAAAGATTAACAATGATGCTGCTGCTGCTGCTG 1000
 DB 1598 GACAGAAAGGCAATACATGCAATGCAAAAGATTAACAATGATGCTGCTGCTGCTGCTG 1657
 QY 1001 TGTCTCTGCTGCTTCTTAATCACTTCAAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1060
 DB 1658 TGTCTCTGCTGCTTCTTAATCACTTCAAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1717

1061 CAGAGACTATGCAACCACTCTCATGTGTGCTCATCTGCGCAGGCTGAGAGCC 1120
1718 CAGAGACTATGCAACCACTCTCATGTGTGCTCATCTGCGCAGGCTGAGAGCC 1777
1121 GCATCCACTGCGCTTCAACGACATTTAGCGTGGAGCTTCAATTTCTGTGATCA 1180
1778 GCATCCACTGCGCTTCAACGACATTTAGCGTGGAGCTTCAATTTCTGTGATCA 1837
1181 AGGATGGGGCCACCGCGGAGGCGCGCTCTGGGCACTTCTCAGGAAACGAGCTCCCT 1240
1838 AGGATGGGGCCACCGCGGAGGCGCGCTCTGGGCACTTCTCAGGAAACGAGCTCCCT 1897
1241 CCTCATCAACAAGCAGTGGCCAGTGGCCGCTCTCAGTTCAGACTGACCACTCCACAG 1300
1898 CCTCATCAACAAGCAGTGGCCAGTGGCCGCTCTCAGTTCAGACTGACCACTCCACAG 1957
1301 GGAAGAGGGGCTTCAACATCACTTTTACCACTTCCGACAAACGAGTCCCGGATCTG 1360
1958 GGAAGAGGGGCTTCAACATCACTTTTACCACTTCCGACAAACGAGTCCCGGATCTG 2017
1361 GGGTTCACATTAATGGCAACCGTTTGGGGAACGCTCCAGCTGGGAGCTCCATCTCT 1420
2018 GGGTTCACATTAATGGCAACCGTTTGGGGAACGCTCCAGCTGGGAGCTCCATCTCT 2077
1421 TCTCTGTATGAGAGCTTCTTGGGACTCAGAGGCTCAGAGACCATCACTGCGCTCTGA 1480
2078 TCTCTGTATGAGAGCTTCTTGGGACTCAGAGGCTCAGAGACCATCACTGCGCTCTGA 2137
1481 AGAGAGGAGAGCTGTCTGGAACAGCGCTGTGCTGGGTGAGAGCTCCCTGTGTGTGTC 1540
2138 AGAGAGGAGAGCTGTCTGGAACAGCGCTGTGCTGGGTGAGAGCTCCCTGTGTGTGTC 2197
1541 ACTGACTTCCGCCACAGCCGCACTCTCTCTCCGGGCTGGCTGCTTCTACAAAGATG 1600
2198 ACTGACTTCCGCCACAGCCGCACTCTCTCTCCGGGCTGGCTGCTTCTACAAAGATG 2257
1601 CCTTGAAGTGTGCTGGGTGATGAGAGCCAGCCAGGCTACCCCATCAAAATCACTTGG 1660
2258 CCTTGAAGTGTGCTGGGTGATGAGAGCCAGCCAGGCTACCCCATCAAAATCACTTGG 2317
1661 ACAGATTCAAAACCGAGGTCATATGACACCTGTGAAGTACGCGATGGGCGGACTTACT 1720
2318 ACAGATTCAAAACCGAGGTCATATGACACCTGTGAAGTACGCGATGGGCGGACTTACT 2377
1721 CAGCGCCCTTGAATCGGGGTTTACCAAGGAAACCGAGGTTCCCGGCTCTCATAGACCA 1780
2378 CAGCGCCCTTGAATCGGGGTTTACCAAGGAAACCGAGGTTCCCGGCTCTCATAGACCA 2437
1781 GCACCTACCT 1840
2438 GCACCTACCT 2497
1841 TCCGCTATGAGACTATATGACATGCACTGACAGACCACTGTCTGATTCAGAGATCCAGTAA 1900
2498 TCCGCTATGAGACTATATGACATGCACTGACAGACCACTGTCTGATTCAGAGATCCAGTAA 2557
1901 ATGGAAGAGGTCATGGGAATGACTTCTAGTGGGCGCGCTGTGACCTTCAAGTGTGACT 1960
2558 ATGGAAGAGGTCATGGGAATGACTTCTAGTGGGCGCGCTGTGACCTTCAAGTGTGACT 2617
1961 CCGGCTACACATTAAGTGAACGAGGAGCTCTGAGAGTGTGAGCCCACTTCCAGTGAAGCC 2020
2618 CCGGCTACACATTAAGTGAACGAGGAGCTCTGAGAGTGTGAGCCCACTTCCAGTGAAGCC 2677
2021 GGGCCCTGCGCAGTGTGAGCTCTGTGTGTGCTTCAATTCAGAGCTCCAGTGGAGCA 2080
2678 GGGCCCTGCGCAGTGTGAGCTCTGTGTGTGCTTCAATTCAGAGCTCCAGTGGAGCA 2737
2081 TCTGTGTGCGCAGGTTCCCTGACTTCTACCCCAAACTTGAACCTGACCTGATATATG 2140
2738 TCTGTGTGCGCAGGTTTCCCTGACTTCTACCCCAAACTTGAACCTGACCTGATATATG 2797
2141 AAACATCTCATGGCAAGGAGTGTCTTCACTTCCACACTTCCAGTGAAGATGGCC 2200

2798 AAACATCTCATGGCAAGGAGTGTCTTCACTTCCACACTTCCAGTGAAGATGGCC 2857
2201 ATGACTACTCTCTCATCATGAGAAAGGAGCTTCAACCCAGCCCTGAGGAGCTAACG 2260
2858 ATGACTACTCTCTCATCATGAGAAAGGAGCTTCAACCCAGCCCTGAGGAGCTAACG 2917
2261 GATCTCGGCTGACAGTCCCATCAGGCGTGGGCTGATAGGCAACTTCACTGCCAGGTCC 2320
2918 GATCTCGGCTGACAGTCCCATCAGGCGTGGGCTGATAGGCAACTTCACTGCCAGGTCC 2977
2321 GCTTCACTCTGATTTCTCATGTATGAGAGATTCACATCACTTCTCAGAGTACG 2380
2978 GCTTCACTCTGATTTCTCATGTATGAGAGATTCACATCACTTCTCAGAGTACG 3037
2381 ACTTGAAGCCCTGTGAGAGCCCGAGGCTCCAGCTTACAGCATTCGGAAGGCTTGCAT 2440
3038 ACTTGAAGCCCTGTGAGAGCCCGAGGCTCCAGCTTACAGCATTCGGAAGGCTTGCAT 3097
2441 TTGGGCTGGGAGACCTTGACCTTCTCTGCTTCCCGGGATACGCTCTGAGGGGACCG 2500
3098 TTGGGCTGGGAGACCTTGACCTTCTCTGCTTCCCGGGATACGCTCTGAGGGGACCG 3157
2501 CCCGATCAGTGTGCTGGGAGGAGAGCGCGCTGTGAGCTCGCTTCCAGAGTGTG 2560
3158 CCCGATCAGTGTGCTGGGAGGAGAGCGCGCTGTGAGCTCGCTTCCAGAGTGTG 3217
2561 TTGCTGAGTGTGGAATTAATGATCAGGCACTCAGGGTACTTTGCTGTCCCCCACTTTC 2620
3218 TTGCTGAGTGTGGAATTAATGATCAGGCACTCAGGGTACTTTGCTGTCCCCCACTTTC 3277
2621 CTGTGAATCAATAATCAATATGATGATGATGATGATGATGATGATGATGATGATGATG 2680
3278 CTGTGAATCAATAATCAATATGATGATGATGATGATGATGATGATGATGATGATGATG 3337
2681 GAATTCAGTGAAGAGCAGGAGCTTGAACCTCTCGAAGAGATGTCTCAAGTGTATG 2740
3338 GAATTCAGTGAAGAGCAGGAGCTTGAACCTCTCGAAGAGATGTCTCAAGTGTATG 3397
2741 ATGGCAACAACACTCCGCCCTTGTCTGGAGATTTTACCATTTCTGATGATGATGATG 2800
3398 ATGGCAACAACACTCCGCCCTTGTCTGGAGATTTTACCATTTCTGATGATGATGATG 3457
2801 TGAATTTGAACAGCATATCAGACAGTGTGATGATTTCACTCATGATGATGATGATG 2860
3458 TGAATTTGAACAGCATATCAGACAGTGTGATGATTTCACTCATGATGATGATGATG 3517
2861 CAGCAAGGAGCTTGTGACATGCACTTTCCAGCTTGAACCTCATCAATGTGAGAACCCAG 2920
3518 CAGCAAGGAGCTTGTGACATGCACTTTCCAGCTTGAACCTCATCAATGTGAGAACCCAG 3577
2921 GAAACCCCAAGTTTGGCTACAAAGTTTATGATGATGATGATGATGATGATGATGATGAT 2980
3578 GAAACCCCAAGTTTGGCTACAAAGTTTATGATGATGATGATGATGATGATGATGATGAT 3637
2981 CCTTCAAGCTGTACCTGTGATACAGCTGCGGAGGATGATGAGAGCTGTGTCTGAGAG 3040
3638 CCTTCAAGCTGTACCTGTGATACAGCTGCGGAGGATGATGAGAGCTGTGTCTGAGAG 3697
3041 GAGAGGCGCGGACTTGGAGACCGGCTCTGCGCACTGTGTCCCGGAGTGTGAGGAGCAAG 3100
3698 GAGAGGCGCGGACTTGGAGACCGGCTCTGCGCACTGTGTCCCGGAGTGTGAGGAGCAAG 3757
3101 TGAAGAGAGAGTGTGCGGAGAGTGTGTCTACCCGAGGATTCAGCTCTCTATGAAACACA 3160
3758 TGAAGAGAGAGTGTGCGGAGAGTGTGTCTACCCGAGGATTCAGCTCTCTATGAAACACA 3817
3161 ATCTCAATGTGACATGTGACATGTGAAAGAGAGGCGGCTGACCAATTTGGGCTACACTTCC 3220
3818 ATCTCAATGTGACATGTGACATGTGAAAGAGAGGCGGCTGACCAATTTGGGCTACACTTCC 3877
3221 TGTGTGTTGACACAGAGAGTTCACAGAGTGTGAGATCTGAGATGAGGCTGTGAGAGA 3280

Db	3878	TCGTTTTCACACAGAGAGCTTACAGAGTCTCCGATCTGGGATGGGCTGTGAGA	3937
QY	3281	GCGGGGTTCTGCTGAAGAGCTGAAGTGCCTGGGCTTCGACAGGACCTGATAGCACT	3340
Db	3938	GCGGGGTTCTGCTGAAGAGCTGAAGTGGCCCGGCTTCGACAGGACCTGATAGCACT	3997
QY	3341	TCAACTCGGTGCTCTGCGAGTTCAGCACTGATTTCTTACAGAGAGAGGGCTTTGGCA	3400
Db	3998	TCAACTCGGTGCTCTGCGAGTTACGACTGACTTTTTCACAGAGAGAGGGCTTTGGCA	4057
QY	3401	TTCAAATTTTCAAGTGTCCACAGAACGTCTCTGCAATGACCTTGGATTCCTGAGATGGGA	3460
Db	4058	TTCAAATTTTCAAGTGTCCACAGCAAGTCTCTGCAATGACCTTGGATTCCTGAGATGGGA	4117
QY	3461	GTCCGAGTGTGTACAGTTTGGGAGAGCCGGGAGACTCCACAGTGTTCACAGTACCTTGCT	3520
Db	4118	GTCCGAGTGTGTGTACAGTTTGGGAGAGCCGGGAGACTCCACAGTGTTCACAGTACCTTGCT	4177
QY	3521	ACGCGCTGCAGGAGAGTGCAGAGATCAGCTGTGTGATGATCGAGAACAGTTCCTTGCGC	3580
Db	4178	ACGCGCTGCAGGAGAGTGCAGAGATCAGCTGTGTGATGATCGAGAACAGTTCCTTGCGC	4237
QY	3581	AGCCAGCCCGCCCAATGCAITGCTGCTCCTGCGGGGAGACCTGACAGAACCATCTGGAG	3640
Db	4238	AGCCAGCCCGCCCAATGCAITGCTGCTCCTGCGGGGAGACCTGACAGAACCATCTGGAG	4297
QY	3641	TCATCCTCTCACCAATTAACCCAGAACCTTACCCGCGAGGAGAGAGTGTACCTGGAAAG	3700
Db	4298	TCATCCTCTCACCAATTAACCCAGAACCTTACCCGCGAGGAGAGAGTGTACCTGGAAAG	4357
QY	3701	TGACCGTCTCACAGACTACGTGATGCGCCCTGGTA--TTTAACTTTTAACCTGGAGC	3757
Db	4358	TGACCGTCTCACAGACTACGTGATGCGCCCTGGTAATTTTCCAGCTTTAACTGGAGC	4417
QY	3758	CTGGCTATGACTTCTCCATATCTACAGAGGAGCGGAGTCTCTCAGCCCTCTCTTAAGAA	3817
Db	4418	CTGGCTATGACTTCTCCATATCTACAGAGGAGCGGAGTCTCTCAGCCCTCTCTTAAGAA	4477
QY	3818	GCTTCTATGCTCCAGCTCCGAGGCGGCATTGAAAGCAGAGACAAGCTTCTCTCG	3877
Db	4478	GCTTCTATGCTCCAGCTCCGAGGCGGCATTGAAAGCAGAGACAAGCTTCTCTCG	4537
QY	3878	CCTTCCGAGAGAGATCTGTGAGCAATGCTGCTTCTGATTTAGCTATACAGAAAC	3937
Db	4538	CCTTCCGAGAGAGATCTGTGAGCAATGCTGCTTCTGATTTAGCTATCCAGAAAC	4597
QY	3938	CGCGGAGTCAATGTTTGTATCTGGTTCATCTAAGAACGCGACACGGGTGGGCTCGACC	3997
Db	4598	CGCGGAGTCAATGTTTGTATCTGGTTCATCTAAGAACGCGACACGGGTGGGCTCGACC	4657
QY	3998	TGAAGCTGGGCTCTCCGCTCACCTATCTGCTCCACGGGGGCTACGAAATTGAGGGACCT	4057
Db	4658	TGAAGCTGGGCTCTCCGCTCACCTATCTGCTCCACGGGGGCTACGAAATTGAGGGACCT	4717
QY	4058	CGACCTGAGCTGATCTCTGGGGGCTGTATGGAAAGCCGCTGTGAACAATCCCGGCGAG	4117
Db	4718	CGACCTGAGCTGATCTCTGGGGGCTGTATGGAAAGCCGCTGTGTGAACAATCCCGGCGAG	4777
QY	4118	TCGTCAGAGCCCCCTGTGGGGGAGATATGTGGATTGCGACGAGTGTCTTGTCCCA	4177
Db	4778	TCGTCAGAGCCCCCTGTGGGGGAGATATGTGGATTGCGAGAGTGTCTTGTCCCA	4837
QY	4178	ACTACCCCAACATCACACAGTGTGAAGATCTGCTTTTGTACTGTGCCCAAG	4237
Db	4838	ACTACCCCAACATCACACAGTGTGAAGATCTGCTTTTGTACTGTGCCCAAG	4897
QY	4238	ACTA--TGTGTGTTTGGCAGTTGCTTCTTTTCAACGGACCTCAACGACGTGGTG	4294
Db	4898	ACTATGTGTGTGTTTGGCAGTTGCTTCTTTTCAACGGACCTCAACGACGTGGTG	4957
QY	4295	AGTTTACAGAGGCAACAGCCAGCATCTGCGGGCTCTCAAGTCTCTCTCGGGCTCCCAAT	4354
Db	4958	AGTTTACAGAGGCAACAGCCAGCATCTGCGGGCTCTCAAGTCTCTCTCGGGCTCCCAAT	5017

QY	4355	CAGGAAGATCACTGCGCCTTGGCACTCCCAATCAAGTTCTCTAATTAAGTTCAACGCCAAG	441
Db	5018	CAGGGAATCACTGCGCTTTGGCACTCCCAATCAAGTTCTAATTAAGTTCAAGCGCAAG	5077
QY	4415	GCGTGCACACAGCCAGAGGCTTCCACTTTGTCTAACAGCGGTTCTCGAACACAGCGCA	4474
Db	5078	GCGTGCACACAGCCAGAGGCTTCCACTTTGTCTAACAGCGGTTCTCGAACACAGCGCA	513
QY	4475	CGCAATGCAGCTCTGTGCCGGAACCCCGCTATGCGAAGAAGCTGGGCACTGACTTCTGG	453
Db	5138	CGCAATGCAGCTCTGTGCCGGAACCCCGCTATGCGAAGAAGCTGGGCACTGACTTCTGG	5197
QY	4535	TGGGGGGCATCGTCCGCTTTCGAAATGCACCTCCGGCTATGCGCTGAGGAGTGCAGAGA	4594
Db	5188	TGGGGGGCATCGTCCGCTTTCGAAATGCACCTCCGGCTATGCGCTGAGGAGTGCAGAGA	525
QY	4595	TCGAGTGCCTCCCTGTGCTGGGGCTTGGCCCAATGGAATGTCTCAGCGCCAGTGTG	4654
Db	5258	TCGAGTGCCTCCCTGTGCTGGGGCTTGGCCCAATGGAATGTCTCAGCGCCAGTGTG	5311
QY	4655	TGGTGCCTGTGGAGGCACTCAACAGGCGCAAGGGACACATCTGTCCCTTGCTTCC	4714
Db	5318	TGGTGCCTGTGGAGGCACTCAACAGGCGCAAGGGACACATCTGTCCCTTGCTTCC	5377
QY	4715	CAGAGCCGTACCTCAACAGCCTCAACTGTGTGTGGAAGATGTGGTCCCGCAAGCGCTG	4774
Db	5378	CAGAGCCGTACCTCAACAGCCTCAACTGTGTGTGGAAGATGTGGTCCCGAAGCGCTG	5433
QY	4775	GCATTCAGATCCAAAGTTGTCAAGTTTGTGACAGAGCAGAACCTGGACTCGCTGAAAT	4834
Db	5438	GCATTCAGATCCAAAGTTGTCAAGTTTGTGACAGAGCAGAACCTGGACTCGCTGAAAT	5497
QY	4835	TTGATGTGAGCATTAACACTGTAACCAATGTCTGGGAGATTCTCAGGAACAACCGTGCCTG	4894
Db	5498	TTGATGTGAGCATTAACACTGTAACCAATGTCTGGGAGATTCTCAGGAACAACCGTGCCTG	5555
QY	4895	CCCTTCTGAAACAGCACTCCAACAGCTCTAACCTTCAATTCTACTCAGATATCAGCGTAT	4954
Db	5558	CCCTTCTGAAACAGCACTCCAACAGCTCTAACCTTCAATTCTACTCAGATATCAGCGTAT	5617
QY	4955	CTGACAGCTGGCTTCACTTGGAGTAACAACGGTGGGCTGAGAGATTTCCGGAACCTG	5014
Db	5618	CTGACAGCTGGCTTCACTTGGAGTAACAACGGTGGGCTGAGAGATTTCCGGAACCTG	5677
QY	5015	CTGTGCCAGTTAACGGGGTGAAGACTGGCGACGCTCACTTGGTAATGATGTGTGTCTT	5074
Db	5678	CTGTGCCAGTTAACGGGGTGAAGACTGGCGACGCTCACTTGGTAATGATGTGTGTCTT	5737
QY	5075	TTCAAGTGTGAACCGGGATATGCGCTCCAGGGGCCAGGCCACATCTTCTGCATGCGCGGAA	5134
Db	5738	TTCAAGTGTGAACCGGGATATGCGCTCCAGGGGCCAGGCCACATCTTCTGCATGCGCGGAA	5797
QY	5135	CAGTGCAGCATGGAATCAACCTCTCTCAACTCTATTTGCAACAGTGTGGGGGAACAGTGG	5194
Db	5798	CAGTGCAGCATGGAATCAACCTCTCTCAACTCTATTTGCAACAGTGTGGGGGAACAGTGG	5857
QY	5195	AGGAGATGAGGGGGTATCTTGAGCCCGGGCTTCCAGGCAACTACCCAGTAATAGG	5254
Db	5858	AGGAGATGAGGGGGTATCTTGAGCCCGGGCTTCCAGGCAACTACCCAGTAATAGG	5917
QY	5255	ACTGCTCTCTGGAATAATGACACTGCCGTGGGCTTTGAGCTCAACATCAGTTCTTGAACT	5314
Db	5918	ACTGCTCTCTGGAATAATGACACTGCCGTGGGCTTTGAGCTCAACATCAGTTCTTGAACT	5977
QY	5315	TCTTCACCGAGCCCAACACAGACTCAATAGAAATCCGGAAATGGCCCTATGAGCAAGCC	5374
Db	5978	TCTTCACCGAGCCCAACACAGACTCAATAGAAATCCGGAAATGGCCCTATGAGCAAGCC	6037
QY	5375	GCATGATGGAAGATTCAGTGGAAGCGAGCTTCCAGCTCCCTCTTCCAGCTGCCAG	5434
Db	6038	GCATGATGGAAGATTCAGTGGAAGCGAGCTTCCAGCTCCCTCTTCCAGCTGCCAG	6097

QY 5435 AGACCAAGGTATTTTCACAGCGACCACTCCAGAAATCGGACGAGATTCAAGTGGAGT 5494
DB 6098 AGACCAAGGTATTTTCACAGCGACCACTCCAGAAATCGGACGAGATTCAAGTGGAGT 6157
QY 5495 ATCAGGCTTATGAATTCAAGAGTGGCCACACCCAGAGCCCTTTGGCAATGGCATTGTGA 5554
DB 6158 ATCAGGCTTATGAATTCAAGAGTGGCCACACCCAGAGCCCTTTGGCAATGGCATTGTGA 6217
QY 5555 GGGAGGTGGCTCAACGTGGGCAATCAGTGAAGCTTGGAGTCCCGGGGGTATCAAT 5614
DB 6218 GGGAGGTGGCTCAACGTGGGCAATCAGTGAAGCTTGGAGTCCCGGGGGTATCAAT 6277
QY 5615 TGAAGTGGCAACCTGTCTCAGTGTCAAGTGGCAACCAACCGGAACTGGGACCAACCC 5674
DB 6278 TGAAGTGGCAACCTGTCTCAGTGTCAAGTGGCAACCAACCGGAACTGGGACCAACCC 6337
QY 5675 TGGCCAAAGTGAAGTCCCTTGGCGGGAACATCATCTTCCCAACGCACTGTGTACT 5734
DB 6338 TGGCCAAAGTGAAGTCCCTTGGCGGGAACATCATCTTCCCAACGCACTGTGTACT 6397
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DB 6398 CCCGGGGTCCCTAGCCGTAATCCAGCTCCAGAGCTGTGTCTGGCTGATGACGCTGC 6457
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QY 5855 TCATCAACATCTGGAGTGGGCAACAGCAACAGCAACGAGCTGGGCTTTCAACCCGGA 5914
DB 6518 TCATCAACATCTGGAGTGGGCAACAGCAACAGCAACGAGCTGGGCTTTCAACCCGGA 6577
QY 5915 GCATGGCCAGAAACAGTGCAGATTCATCAACAGGCTCCGCTCAATTCACACCTGC 5974
DB 6578 GCATGGCCAGAAACAGTGCAGATTCATCAACAGGCTCCGCTCAATTCACACCTGC 6637
QY 5975 ATCAGGCAACAGGGGGATCTTGCATAGCTTCTCCGCTTATCCACTCACCAGATGCC 6034
DB 6638 ATCAGGCAACAGGGGGATCTTGCATAGCTTCTCCGCTTATCCACTCACCAGATGCC 6697
QY 6035 CTCTCCACCATCTCTCCCAACGCGAGTGTGTCAAGAAATGAAGATTCATATAG 6094
DB 6698 CTCTCCACCATCTCTCCCAACGCGAGTGTGTCAAGAAATGAAGATTCATATAG 6757
QY 6095 GTGCAATCGTACGCTCAGATGCTCTCCGCTTATCCACTAGTGGGAAATGAATTCGA 6154
DB 6758 GTGCAATCGTACGCTCAGATGCTCTCCGCTTATCCACTAGTGGGAAATGAATTCGA 6817
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DB 6818 CTTGCAAACTTGGAACTTACCTGCAAGTGAAGGACCAACCCGATATGTGAAGTGAAGT 6877
QY 6215 GTTCAACAAATGAAGTCTTGAAGACTCAACAGGCTGTCTGAGCCAGAGTACCTGC 6274
DB 6878 GTTCAACAAATGAAGTCTTGAAGACTCAACAGGCTGTCTGAGCCAGAGTACCTGC 6937
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DB 6938 GAAGCATATCCCGATTCAGAACTGTCTGTGGGTGGAGAGTGGAGCCGCACTATTAACA 6997
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DB 7058 ATGATTCATCAGAGCAGAGTCTCTGTGAAAGCCCTCAGTGGAAATTAATCAGCTCCC 7117
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DB 7178 ATCGAAGGGCTTCAAGATCCGCTATTCAGCCCTTACTGACAGCTGGCCAGGGCTCAC 7237
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DB 7238 TCCATGGCTTATCCTTGAAGCAGACCAAGCAACCCAGCCGGGGCTCATCTTTGGCT 7297
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DB 7298 GCAAGCCGGCTTACCCCTGGTGGGACAGCATGTGCTGTACCCGCAACCCGAG 7357
QY 6695 GCTTACCACTGTGAGAGCAAGCCATCCCTCTGTGCAAGCTCTTTCCTGTGGCTTCTG 6754
DB 7358 GCTTACCACTGTGAGAGCAAGCCATCCCTCTGTGCAAGCTCTTTCCTGTGGCTTCTG 7417
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DB 7538 ACAGAGGCTTATGAGCAACCGCAATGTCCACACAGTGTGTCCCTGTGACTTGTCTG 7597
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DB 7598 ATGTCAATGATCAGCTGTGAGAGCATGAGCCGATGAGGCTTATCTTTGAGACAGTATC 7657
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QY 7055 TCATCCGCTGTGAGGCAATGCAATGAGGCTCGGGGACTTCAAGCCCACTGCGGA 7114
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QY 7115 TCATCTCTGTGAGAGCTCCGATTCGCCCAATGGCCACCGCATGGAACATGTCTG 7174
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DB 7898 TGGGTAGTGAAGGCAATGGGCTTGGAGTGGCTCTGAAGTCCGCTGCTGTGAGC 7957
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DB 8138 GACACCCAGGCAACCTGTCAACGCGCTCACTCAGGATACCAAGTTAACTTCAAGATG 8197
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DB 8198 TGGTCAAGTTGTTGCAACCCCTGGGTATATGCTGAGGGGCTGTAGTCCCAATGGC 8257
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QY 8195 GGAACCTGTGGGACTCCAGTAATGCGGAGTGTGTTCAGTATGAGCTGTGTTTCTCA 8254
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QY 8375 ACCCTGGATTCAGGCAATGAGCTTCCGCTGGGCAATGATCTTCAAGTAAACAACAATG 8434
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QY 8615 TGAACATATAGTGTGTCTCTGCTTATGATGGAAGTCAATAGAGTATCTGTGTGACT 8674
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QY 9035 CAAACCTGACCTGGAATGGAACCCCACTGATGTGTGTGTGTGTGTGTGTGTGTGTGTGT 9094
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 DB 10538 GGGCCACATTTTGAAGACCCCAATGATGACGCGCAACATCCAGCCCAAGACATATGCGCA 10597
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RESULT 7
 ADH71143
 ID ADH71143 standard; DNA: 10466 BP.
 AC ADH71143;
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 DT 25-MAR-2004 (first entry)
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 DE Human gene of the invention NOV4e SEQ ID NO:39.
 XX
 KW ds; gene; human; cytosolic; immunomodulator; neuroprotective; nootropic;
 KW anorectic; antidiabetic; antimicrobial; antilipemic; gene therapy;
 KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
 KW obesity; diabetes; infectious disease; metabolic syndrome X;
 KW dyslipidaemia.
 OS Homo sapiens.
 XX
 PN WO2003102155-A2.
 XX
 PD 11-DEC-2003.
 XX
 PF 03-JUN-2003; 2003WO-US017430.
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 PR 03-JUN-2002; 2002US-0385120P.
 PR 04-JUN-2002; 2002US-0385784P.
 PR 05-JUN-2002; 2002US-0386041P.
 PR 06-JUN-2002; 2002US-0386047P.
 PR 06-JUN-2002; 2002US-0386453P.
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PR 17-JUN-2002; 2002US-0389742P.
 PR 18-JUN-2002; 2002US-0389848P.
 PR 19-JUN-2002; 2002US-0390006P.
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 PR 21-JUN-2002; 2002US-0390763P.
 PR 17-JUL-2002; 2002US-0396706P.
 PR 06-AUG-2002; 2002US-0401628P.
 PR 09-AUG-2002; 2002US-0402156P.
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 PR 12-AUG-2002; 2002US-0402821P.
 PR 12-AUG-2002; 2002US-0402832P.
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 PR 13-AUG-2002; 2002US-0403531P.
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 PR 13-AUG-2002; 2002US-0406117P.
 PR 15-AUG-2002; 2002US-0406117P.
 PR 26-AUG-2002; 2002US-0418282P.
 PR 26-AUG-2002; 2002US-0406355P.
 PR 27-AUG-2002; 2002US-0406240P.
 PR 20-SEP-2002; 2002US-041528P.
 PR 23-SEP-2002; 2002US-041731P.
 PR 30-SEP-2002; 2002US-0414801P.
 PR 30-SEP-2002; 2002US-0414839P.
 PR 30-SEP-2002; 2002US-0414840P.
 PR 30-SEP-2002; 2002US-0414954P.
 PR 09-OCT-2002; 2002US-0417186P.
 PR 09-OCT-2002; 2002US-0417406P.
 PR 23-OCT-2002; 2002US-0420639P.
 PR 28-OCT-2002; 2002US-0421136P.
 PR 31-OCT-2002; 2002US-0422690P.
 PR 01-NOV-2002; 2002US-0423130P.
 PR 05-NOV-2002; 2002US-00423798.
 PR 05-NOV-2002; 2002US-0423798P.
 PR 12-NOV-2002; 2002US-0425453P.

(CURA-) CURAGEN CORP.
 XX
 PA
 XX
 PI Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
 PI Caterton E, Chapoval EA, Crabtree-Bokor JR, Edinger SR, Ellerman K;
 PI Ectenberg S, Gangoli EA, Gerlach VP, Gorman L, Gunther E, Guo X;
 PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR,
 PI Macdougall T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
 PI Padigar M, Paturnajan M, Pena CA, Peyman JA, Raha D, Rastelli L;
 PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;
 PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
 PI Zhong H;
 DR
 DR
 DR
 DR
 PT
 PT
 XX
 XX
 PS
 PS
 CC The invention relates to a novel isolated polypeptide (NOVX). A
 CC polypeptide of the invention has cytosolic, immunomodulator,
 CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
 CC antilipemic activity, and may have a use in gene therapy, and as a
 CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
 CC any of the 303 fully defined nucleotide sequences given in the
 CC specification. The polypeptide is useful in the manufacture of a
 CC medicament for treating a syndrome associated with a human disease. The
 CC polypeptide, polynucleotide and antibody are useful in diagnosing,
 CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
 CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious

QY 2141 AACATCTCATGGCAAGGTGTGTCTTCACTTTCACACCTTCCACCTTGGAAAGTGGCC 2200
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Db 2918 GATCTGGGCTGCCAGCTCCCATCAAGCCTGGGCTCTATGGCAACTTCACTGCCAGGTCC 2977
QY 2321 GCTTCACTCTGATTTCTCCATGTCATATGAAAGGATTCACATCACTTCTCAGAGTACG 2380
Db 2978 GCTTCACTCTGATTTCTCCATGTCATATGAAAGATTCACATCACTTCTCAGAGTACG 3037
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Db 3038 ACTTGAAGCCTCTGAGAGACCCGAGGTCCAGCTTACAGCATCCGGAAGGCTTGCAGT 3097
QY 2441 TTGGCGTGGGCGACACTTGAACCTTCTCTGCTTCCCGGGTACCGTCTGAGAGGCACTG 2500
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6698 CTCTCCCAACCATCTCCCAACGCGAAGTGTACAGAGAAATGAATTAATATAG 6757
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6335 TCTGCTCAGAGTGTAGTACTTCTCAGCGAGAGCAATATGATGAGTTGAGATTTTGG 6394
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6395 ATGTGTCAATCAGAGCAGAGTCTCTGCTGAAGGCTTCAAGTGGAAATTAATCACTCCG 6454
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6455 TGATTTGACAGGCTCAAGCAACTCTGTGTACTGTGACTGTGTGTGTGTGTGTGTGTGTGT 6514
7118 TGATTTGACAGGCTCAAGCAACTCTGTGTACTGTGACTGTGTGTGTGTGTGTGTGTGTGT 7177

QY	6515	TTCCGAAGGGGCTTCAAGATCCGCTATTTCAGGCCCCCTTACTGACAGCTGCCAAGGGTCCAC	65174
Db	7178	ATCCGAAGGGCTTCAAGATCCGCTATTTCAGGCCCCCTTACTGACAGCTGCCAAGGGTCCAC	7209
QY	65175	TCATATGGCTTCACTCTAGGCCAGACCAAGCACCAGGCCGAGGGGCTCCATCCACTTGGCT	6634
Db	7210	-----	7209
QY	6635	GCAAGCGGGGCTACCGCCTGGTGGGACACAGCATGGCCATCTGATCCGGACCCCCAGG	6694
Db	7210	-----	7209
QY	6695	GCTACCACTGTGAGAGCGAAGCCATCCCTCTCTGTCAGACTCTTTCCTGTGGGCTTCGTG	6754
Db	7210	-----CTTTCCTGTGGGCTTCGTG	7228
QY	6755	AGGCCCCCAAGATGGAAATGGTGTGGCCAAAGAGTACACAGTGGGAACCAAGCGCTGT	6814
Db	7229	AGGCCCCCAAGATGGAAATGGTGTGGCCAAAGAGTACACAGTGGGAACCAAGCGCAATG	7288
QY	6815	ACAGCTGACATGAAGGCTTACCACTCCAGGGAGGGGCTGAGGCGCATCTGACAGTGTCTGG	6874
Db	7289	ACAGCTGACATGAAGGCTTACCACTCCAGGGAGGGGCTGAGGCGCATCTGAGGCTCTGG	7348
QY	6875	ACACAGGCTTATGAGCAACCGCAATGTCCACCAAGTGTGTCCCTGTGACTTGTCTGTG	6934
Db	7349	ACACAGGCTTATGAGCAACCGCAATGTCCACCAAGTGTGTCCCTGTGACTTGTCTGTG	7408
QY	6935	ATGTACATATGATCATCAGCGTGGAGCATGGCCGATGGAGGCTTATCTTTAGACACATATC	6994
Db	7409	ATGTACATATGATCATCAGCGTGGAGCATGGCCGATGGAGGCTTATCTTTAGACACATATC	7468
QY	6995	AGTTCCAGAGCCAGCTGATGTGCATCTGTGACCTGTGGCTACTACTATCTAGGCCAAAGG	7054
Db	7469	AGTTCCAGAGCCAGCTGATGTGCATCTGTGACCTGTGGCTACTACTATCTAGGCCAAAGG	7528
QY	7055	TCATTCGCTGTACAGGCCAATGGCAAAATGAGCTTCGGGAGCTCTACGCCCACTTGGCGAA	7114
Db	7529	TCATTCGCTGTACAGGCCAATGGCAAAATGAGCTTCGGGAGCTCTACGCCCACTTGGCGAA	7588
QY	7115	TCATCTCCGTGGAGAGGCTCCCGATTTCCGCCCAATGGGCAACCGCATGGGAACACTGTCTG	7174
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QY	7235	TGCGTGAATGCATGGCCCAATGGGCTCTGGAATGGCTCTGGAAGTCCGCTGCTTGTGTGAC	7294
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QY	7295	ACTGTGGGACTCCTAGGCCCATTTGTGCAACGGACATCATATGGGGAGAACTACAGCTTAC	7354
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QY	7415	TCGTGCACACAGATATCATCTGTGTGGGCAAGACCCCTTTCGTGTGCAATTCCTGTG	7474
Db	7889	TCGTGCACACAGATATCATCTGTGTGGGCAAGACCCCTTTCGTGTGCAATTCCTGTG	7948
QY	7475	GACACCCAGGCAACCTGTGCAACGGGCTCACTCAGAGGTAAACAGTTTAACTCAACGATG	7534
Db	7949	GACACCCAGGCAACCTGTGCAACGGGCTCACTCAGAGGTAAACAGTTTAACTCAACGATG	8008
QY	7535	TGCTCAAGTTTGTTCGAACCTCGGGTATATGGCTGAGGGGGCTGTAGTGTCCAGTACC	7594
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QY	7595	TGGCAGGCGGCATATGGATGTGACATGCTGCCACCTGTGAGAAATATCAATCAATGTAACAGATC	7654
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QY	7655	CTGGACACCAAGAAATAGTGTTCGTGACAGGTCCACGCGCAGCGGCCTGCACAGTTACACT	7714
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QY	7715	TGGGCAACCACTGTGTCTTAAACCGGTGCACAACACGGCTTCTACCTCTGTGGGCAACCCAGTGC	7774
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Db	8249	TCAGTGTCCAGGGAGATGGGCACATGGGACCGTCCCGCGCCCAAGTGTCTGTGGTGTCT	8308
QY	7835	GTGGCCATCCCGGGCTCCCGCTCTCACTCCAGATGTGTGGAGACATTTATCTGTGGAG	7894
Db	8309	GTGGCCATCCCGGGCTCCCGCTCTCACTCCAGATGTGTGGAGACATTTATCTGTGGAG	8368
QY	7895	CAGTGTGCGGTACGTGATGCGGCAACGCTACTTGTGTGGAAACAGCACCCGATGT	7954
Db	8369	CAGTGTGCGGTACGTGATGCGGCAACGCTACTTGTGTGGAAACAGCACCCGATGT	8428
QY	7955	GTGGGCTGGATGGACATCTGACCTGGCTCCCTCCCTCACTGTCACAGAACACGCGTGGGAG	8014
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QY	8015	TTTGGCGGTGACCCCTGGGGATCCCGGCTCATGGCATCCGTTTGGGGGACAGCTTTGATCAG	8074
Db	8489	TTTGGCGGTGACCCCTGGGGATCCCGGCTCATGGCATCCGTTTGGGGGACAGCTTTGATCAG	8548
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Db	8549	GCACTGTGATGCGCTTCAGCTGTGAAGCTGGCCACAGTCTTCGGGGGATGTGTACAGGCGCA	8608
QY	8135	CCTGTCAAGCCAAATGGCTCTGTGGAGCGGCTTCGACGCTGTAGTGTGGATGATCTCTTGTG	8194
Db	8609	CCTGTCAAGCCAAATGGCTCTGTGGAGCGGCTTCGACGCTGTAGTGTGGATGATCTCTTGTG	8668
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QY	8255	GCTCTATGCTATAGATGCCGGGAGGATCTACGCGCACAGGCTGTCTCAGCCGTCACCT	8314
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QY	8315	GCTCGGTCAATGGTACTGTGACAGGCGAGTGACCTTGATGTGCTGTCTATATACTGTGGTG	8374
Db	8789	GCTCGGTCAATGGTACTGTGACAGGCGAGTGACCTTGATGTGCTGTCTATATACTGTGGTG	8848
QY	8375	AACCTGGGATATCCACGCCAATGGGCTTTGGGCTGGGGCAATGACTTCAGGTAACAACAACTG	8434
Db	8849	AACCTGGGATATCCACGCCAATGGGCTTTGGGCTGGGGCAATGACTTCAGGTAACAACAACTG	8908
QY	8435	TGACATATCAGTGTGCCCTGGCTATATGATGAGTGCACATAGAGTATCTGTGCTGAGCT	8494
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QY	8495	GCACCAAGAGACCGGACATGGATGGAAACAAAGCCCGTCTGCAAAAGCTTCAATGTGCAGC	8554
Db	8969	GCACCAAGAGACCGGACATGGATGGAAACAAAGCCCGTCTGCAAAAGCTTCAATGTGCAGC	9028
QY	8555	CACCTCCGCTATATCCCAATGGGAAAGGTGTGGGGTGTGACTTCAATGTGGGCTCAAGTG	8614
Db	9029	CACCTCCGCTATATCCCAATGGGAAAGGTGTGGGGTGTGACTTCAATGTGGGCTCAAGTG	9088
QY	8615	TGACTTATGCTGCTGGAGGGGTACACAGCTCTCCCTGCCGCGGCTTTCACTCTGTAGG	8674
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Db      9149 GAAATGGGTCCTGGACCGGAGAGCTGCCTCAGTGTTCCTCTGTGTTCTCGGGAGTCTCTG 9208
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Qy      9334 CCAGAAATTCCTGTGGAAAGGGGCTATGATATACAGGGGAGAAAGACGAGCCATGAC 9393
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Qy      9394 TCAGAGTACTGCTTCCAAAGTTGCCAAGAGGTCAATGSCAATGATGACACCA 9453
Db      9869 TCAGAGTACTGCTTCCAAAGTTGCCAAGAGGTCAATGSCAATGATGACACCA 9928
Qy      9454 GTGGGTGGAGTGCATCTGTGTGGAACCTTAAAGAAAGAAATTTCTCTCTCACTCC 9513
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Qy      9634 CTGTCAAGGGCCCAAGGCTTTGGGAGTGTGGCTTTCAAGATCTGACAGCTGTCTGG 9693
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Qy      9934 GCGAGGGGAGTGTACAGTACAGCAGTGTGACAGACAGATTAAGCCACCCGGCTTGGC 9991
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RESULT 8
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ID ADH71145 standard; DNA, 12900 BP.
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AC ADH71145;
XX
DT 25-MAR-2004 (first entry)
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DE Human gene of the invention NOV4E SEQ ID NO:41.
XX
KW ds; gene; human; cytosolic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antipneumatic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.
XX
OS Homo sapiens.
XX
PN W02003102155-A2.
XX
PD 11-DEC-2003.
XX
PE 03-JUN-2003; 2003WO-US017430.
XX
PR 03-JUN-2002; 2002US-0385120P.
PR 04-JUN-2002; 2002US-0385784P.
PR 05-JUN-2002; 2002US-0386041P.
PR 06-JUN-2002; 2002US-0386047P.
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PR 14-JUN-2002; 2002US-0389118P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389144P.

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PR 14-JUN-2002; 2002US-0389149P.
 PR 17-JUN-2002; 2002US-0389726P.
 PR 17-JUN-2002; 2002US-0389742P.
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 PR 17-JUL-2002; 2002US-0396706P.
 PR 06-AUG-2002; 2002US-0401628P.
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 PR 28-OCT-2002; 2002US-0421156P.
 PR 31-OCT-2002; 2002US-0422690P.
 PR 01-NOV-2002; 2002US-0423130P.
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 PR 12-NOV-2002; 2002US-0425453P.
 PR
 PA (CPRA-) CBRAGEN CORP.
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 PI Alsebrook JP, Alvarez E, Anderson DM, Boldog FL, Casman SJ;
 PI Catereron E, Chappoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
 PI Ettenberg S, Gangoli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
 PI Guev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, MacDougall JR;
 PI Macclachlan T, Malayakar UM, Mezick AJ, Millet I, Mishra VS;
 PI Padiganu M, Paturajan M, Pena CBA, Peyman JA, Raha D, Rastelli L;
 PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shinkets RA;
 PI Smithson G, Spytek KA, Stone DJ, Vermet CM, Voss EZ, Zhong M;
 PI Zhong H;
 XX
 XX WPI; 2004-081935/08.
 DR P-PsDB; ADH71146.
 DR
 XX
 PT New NOXV polypeptides and nucleic acid molecules useful for preventing or
 PT treating NOXV-associated disorders, e.g. cancer, diabetes, infection or
 PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
 XX
 XX
 PS Example 4; SEQ ID NO 41; 1880pp; English.
 CC
 CC The invention relates to a novel isolated polypeptide (NOXV). A
 CC polypeptide of the invention has cytostatic, immunomodulator,
 CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
 CC antipneumatic activity, and may have a use in gene therapy, and as a
 CC vaccine. The polypeptides are encoded by NOXV polynucleotides comprising
 CC any of the 303 fully defined nucleotide sequences given in the
 CC specification. The polypeptide is useful in the manufacture of a
 CC medicament for treating a syndrome associated with a human disease. The
 CC medicament for treating a syndrome associated with a human disease. The
 CC polypeptide, polynucleotide and antibody are useful in diagnosing,

Query Match	Best Local Similarity	86.4%; 94.2%;	Score 8760.4;	Pred. No. 0;	DB 12;	Length 12900;	Mismatches 121;	Indels 458;	Gaps 7;
101	AGCTAGTCANAGAACCAATTGAGTGAAGTTCGAGGTGGAAGCTGTAATGCCAGCAAG	160							
842	ACCAAGTCMAAMACCAATTGATGTAAGTCTTCAGGGTGAAGCTGATGCGCCAGCAAG	901							
161	ACAACAGCCAGAAACGCTGTGTGTTAACTCAGTGTGTTGTGCCAAGACATATATGT	220							
902	ACAACAGCCAGAAACGCTGTGTGTTAACTCAGTGTGTTGTGCCAAGACATATATGT	961							
221	GTCCAGACCTCTGGCATACCCGGAAGGGGCAAAAGCTAGAGCTCGGATTTACGTTAGAT	280							
962	GTCCAGACCTCTGGCATACCCGGAAGGGGCAAAAGCTAGAGCTCGGATTTACGTTAGAT	10212							
281	CCAGCGTCGCAATTCACCTGCAACGAGGCTATGACCTGCAAGGGTCCAGGCGATACCT	340							
1022	CCAGCGTCGCAATTCACCTGCAACGAGGCTATGACCTGCAAGGGTCCAGGCGATACCT	1081							
341	GTATGAAAGTAGGCGACATGTTTTCGCGCTGAGACGACACAGGCGCAGTCTGCCAGGCC	400							
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461	TTTCAGTATGACAAACAAAGGACACGCTGTGTGATCATACAGCACTCAACCCCTCAAG	520							
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701	GGCAGAAATGACCTGTACTTGAGATCTGTCTGTGACATTTAGCAGTTTCAGATGCAAGT	760							
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761	GTTCAGTAGGAAGCTCTCCAAAGACTTCTTAATGCTGTGAACTGTTGCTCTCTGGACAG	820							
1418	GTTCAGTAGGAAGCTCTCCAAAGACTTCTTAATGCTGTGAACTGTTGCTCTCTGGACAG	1477							
821	AGATCGAGCAGGGAGTGGGGGTACCTGTGCATACCTGCATATGCGCGAGGGAAAGCT	880							
1478	AGATCGAGCAGGGAGTGGGGGTACCTGTGCATACCTGCATATGCGCGAGGGAAAGCT	1537							
881	CCCGGATTTCAACACGCTGACACACTCAAGTTTGAATGCAAGCCGCGCTTTGAGCTGTG	940							
1538	CCCGGATTTCAACACGCTGACACACTCAAGTTTGAATGCAAGCCGCGCTTTGAGCTGTG	1597							
941	GACGAAAGGACATCACTGCGCAAAAGATTAACAATGTGTGCGCTTAAGAAGCAGAGCTCG	1000							
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 DB 2018 GCGTTCAGTAATGACAAACGATTTGGAGACAGCTCCAGCTGAGGCACTCATCTCCT 2077
 QY 1421 TCTCTGTGATGAAGCTTCTTGGAGCTCAGAGGCTCAGAGACATCACTTGTGCTTGA 1480
 DB 2078 TCTCTGTGATGAAGCTTCTTGGAGCTCAGAGGCTCAGAGACATCACTTGTGCTTGA 2137
 QY 1481 AGAAGAGGACCGTGTCTGAAACAGCGCTGTGCGGTGAGTGAAGCTCCTGTGAGTGC 1540
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 QY 1541 ACCTGACTTCCGCGACGCGCACCATCTCTCCGAGCTGAGCTTCTTCAAGAGATG 1600
 DB 2198 ACCTGACTTCCGCGACGCGCACCATCTCTCCGAGCTGAGCTTCTTCAAGAGATG 2257
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 DB 2498 TCCGATATGAGACTATPAACACTGACAGACCACTGTCTGATCCAGAGATCCCACTPA 2557
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 DB 2558 ATGAGCAGCGTCAATGGAAATGACTTTCACGTGGCGGCTGTGACTTCACTGTGACT 2617
 QY 1961 CCGGCTTACATTTAATGACGAGGAGCTTGTGAAGTGAAGCCCACTTCCAGTGAAGC 2020
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DB 2738 TCTTGTGCGCAAGGTTCCCTGACTTCAACCCCAACATTTGAATGACCTGGAATATGCG 2797
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 DB 2798 AAACATCTCATGGAAGGAGTGTCTTCACTTCCACACTTCCACCTGGAAGTGGCC 2857
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RESULT 9

ADH71139
ID ADH71139 standard; DNA; 8010 BP.

XX ADH71139;

DT 25-MAR-2004 (first entry)

DE Human gene of the invention NOV4c SEQ ID NO:35.

XX ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
XX anorectic; antidiabetic; antimicrobial; antileptemic; gene therapy;
XX vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
XX obesity; diabetes; infectious disease; metabolic syndrome X;
XX dyslipidaemia.

OS Homo sapiens.

XX MO2003102155-A2.

XX 11-DEC-2003.

PF 03-JUN-2003; 2003MO-US017430.

PR 03-JUN-2002; 2002US-0385120P.

PR 04-JUN-2002; 2002US-0385784P.

PR 05-JUN-2002; 2002US-0386041P.

PR 06-JUN-2002; 2002US-0386047P.

PR 06-JUN-2002; 2002US-0386376P.

PR 06-JUN-2002; 2002US-0386453P.

PR 06-JUN-2002; 2002US-0386864P.

PR 07-JUN-2002; 2002US-0387016P.

PR 07-JUN-2002; 2002US-0386796P.

PR 07-JUN-2002; 2002US-0386816P.

PR 07-JUN-2002; 2002US-0386931P.

PR 07-JUN-2002; 2002US-0386942P.

PR 07-JUN-2002; 2002US-0386971P.

PR 07-JUN-2002; 2002US-0387262P.

PR 08-JUN-2002; 2002US-0296960P.

PR 10-JUN-2002; 2002US-0387400P.

PR 10-JUN-2002; 2002US-0387535P.

PR 11-JUN-2002; 2002US-0387610P.

PR 11-JUN-2002; 2002US-0387625P.

PR 11-JUN-2002; 2002US-0387634P.

PR 11-JUN-2002; 2002US-0387668P.

PR 11-JUN-2002; 2002US-0387702P.

PR 11-JUN-2002; 2002US-0387836P.

PR 11-JUN-2002; 2002US-0387859P.

PR 12-JUN-2002; 2002US-0387933P.

PR 12-JUN-2002; 2002US-0387934P.

PR 12-JUN-2002; 2002US-0387960P.

PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.
PR 13-JUN-2002; 2002US-0389123P.
PR 14-JUN-2002; 2002US-0389118P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389144P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389729P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389844P.
PR 19-JUN-2002; 2002US-0390006P.
PR 19-JUN-2002; 2002US-0390209P.
PR 21-JUN-2002; 2002US-0390763P.
PR 17-JUL-2002; 2002US-039706P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402156P.
PR 09-AUG-2002; 2002US-0402256P.
PR 09-AUG-2002; 2002US-0402389P.
PR 12-AUG-2002; 2002US-0402786P.
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PR 13-AUG-2002; 2002US-0403532P.
PR 13-AUG-2002; 2002US-0403563P.
PR 15-AUG-2002; 2002US-0406317P.
PR 15-AUG-2002; 2002US-0406317P.
PR 26-AUG-2002; 2002US-0406182P.
PR 26-AUG-2002; 2002US-0406355P.
PR 27-AUG-2002; 2002US-0406240P.
PR 12-SEP-2002; 2002US-0410084P.
PR 20-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
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PR 30-SEP-2002; 2002US-0414954P.
PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417166P.
PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-0423798P.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.

(CURA-) CURAGEN CORP.

XX Albrock JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
XX Cateron E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K,
XX Ettenberg S, Gangoli BA, Gerlach VL, Gorman L, Gunther E, Guo X,
XX Guev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, MacDougall JR,
XX MacLachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
XX Padigan M, Paturajan M, Pena CE, Peyman JA, Raha D, Raetzell L,
XX Ridger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;
XX Smithson G, Spytek KA, Stone DJ, Vernet CM, Voss EZ, Zhong M,
XX Zhong H;

WP1; 2004-081935/08.

DR P-PSDB; ADH71140.

XX New NOV4c polypeptides and nucleic acid molecules useful for preventing or

PT treating NOV4c-associated disorders, e.g., cancer, diabetes, infection or

XX obesity, and in chromosome mapping, tissue typing or pharmacogenomics.

XX Example 4; SEQ ID NO 35; 1880bp; English.

CC The invention relates to a novel isolated polypeptide (NOV4c). A

CC polypeptide of the invention has cytostatic, immunomodulator,

CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and

781 AAGACTTATGCTGTGGAATTGTTGCTCTGGGACAGATCGAGCAGGCGAATTGC 840

[illegible]

QY 1921 GACTTCTAAGTGGGCGCGCTGTGTGACTTCAAGCTGTGACTCGGCGCTACACATTAAGTAC 1980
Db 1921 GACTTCTAAGTGGGCGCGCTGTGTGACTTCAAGCTGTGACTCGGCGCTACACATTAAGTAC 1980
QY 1981 GGGGAGCGCTCTGAGTGTGAGCCCACTTCCAGTGAAGCCGGGCGCTCCAGTGTGAA 2040
Db 1981 GGGGAGCGCTCTGAGTGTGAGCCCACTTCCAGTGAAGCCGGGCGCTCCAGTGTGAA 2040
QY 2041 GCTCTCTGTGTGTGCTTCAATTCAGGCTTCAAGTGGGACCATCTTGTCCGCAAGGTTCCCT 2100
Db 2041 GCTCTCTGTGTGTGCTTCAATTCAGGCTTCAAGTGGGACCATCTTGTCCGCAAGGTTCCCT 2100
QY 2101 GACTTCTAAGCCCAACATTTGAATGTGACCTGTGATTAATGAAACATTCATGAGGAGGT 2160
Db 2101 GACTTCTAAGCCCAACATTTGAATGTGACCTGTGATTAATGAAACATTCATGAGGAGGT 2160
QY 2161 GTGTTCTTCACTTCCACACTTTCACACTGTGAAGTGGCATGACTTACCTCTCATCACT 2220
Db 2161 GTGTTCTTCACTTCCACACTTTCACACTGTGAAGTGGCATGACTTACCTCTCATCACT 2220
QY 2221 GAGAAAGGAGCTTCAACCCAGCCCTGAGGAGCTTACCTGATCTGCGCTGCACTGCC 2280
Db 2221 GAGAAAGGAGCTTCAACCCAGCCCTGAGGAGCTTACCTGATCTGCGCTGCACTGCC 2280
QY 2281 ATCAGCGCTGGGCTCTATGAGCACTTCACTGCGCGAGTCCGCTTCACTCTGATTTCC 2340
Db 2281 ATCAGCGCTGGGCTCTATGAGCACTTCACTGCGCGAGTCCGCTTCACTCTGATTTCC 2340
QY 2341 ATGCTATATGAAGATTCAACATCACTTCTCAGATGACAGCTTGAAGCCCTGTGAGAG 2400
Db 2341 ATGCTATATGAAGATTCAACATCACTTCTCAGATGACAGCTTGAAGCCCTGTGAGAG 2400
QY 2401 CCCGAGGTCCAGCTCAACAGCATCCGGAAGGGCTTGCAGTTGGGTGGGCGACACTTG 2460
Db 2401 CCCGAGGTCCAGCTCAACAGCATCCGGAAGGGCTTGCAGTTGGGTGGGCGACACTTG 2460
QY 2461 ACCCTTCTCTGCTCCCGGGGTACCGTCTGAGGGGACCGCCGCACTCAGTGGCGAG 2520
Db 2461 ACCCTTCTCTGCTCCCGGGGTACCGTCTGAGGGGACCGCCGCACTCAGTGGCGAG 2520
QY 2521 GGCAGAGCGGCGCTGTGAGCTCGCTCTGCAAGGTGTGTGCTGAGTGTGGAAATTC 2580
Db 2521 GGCAGAGCGGCGCTGTGAGCTCGCTCTGCAAGGTGTGTGCTGAGTGTGGAAATTC 2580
QY 2581 GTCAAGGAGCTCAAGGTACTTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2640
Db 2581 GTCAAGGAGCTCAAGGTACTTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2640
QY 2641 CATGAATGATCTCACTCCATCCAGACCCAGCCAGGGAAGGAATTCAGCTGAAGCCAGG 2700
Db 2641 CATGAATGATCTCACTCCATCCAGACCCAGCCAGGGAAGGAATTCAGCTGAAGCCAGG 2700
QY 2701 GCAATTCGAATCTCTCGAAGAGATGTCTCAAGTTTATGATGCAACAACTCCGCC 2760
Db 2701 GCAATTCGAATCTCTCGAAGAGATGTCTCAAGTTTATGATGCAACAACTCCGCC 2760
QY 2761 GATTTCGAATCTCTCGAAGAGATGTCTCAAGTTTATGATGCAACAACTCCGCC 2820
Db 2761 GATTTCGAATCTCTCGAAGAGATGTCTCAAGTTTATGATGCAACAACTCCGCC 2820
QY 2821 AGCAGCTGTGCTGATTTCACTCACTGATGCTGAAGAACACAGCAAGGCTTTGAACCTG 2880
Db 2821 AGCAGCTGTGCTGATTTCACTCACTGATGCTGAAGAACACAGCAAGGCTTTGAACCTG 2880
QY 2881 CACTTTTCAGCTTTGAATCTCAATTAATGAGAACCCAGAACTTGTGGCTAC 2940
Db 2881 CACTTTTCAGCTTTGAATCTCAATTAATGAGAACCCAGAACTTGTGGCTAC 2940
QY 2941 AAGCTTCAGTGAAGTGAAGTGAAGGAGGAGTCCGTCTGAGCTGTGAGCCCTGGA 3000
Db 2941 AAGCTTCAGTGAAGTGAAGTGAAGGAGGAGTCCGTCTGAGCTGTGAGCCCTGGA 3000

QY 3001 TACAGCTGCGGGGTAGTGAAGAGCTGTGTGTGATGAGAGAGCCCGGACCTGGGAC 3060
Db 3001 TACAGCTGCGGGGTAGTGAAGAGCTGTGTGTGATGAGAGAGCCCGGACCTGGGAC 3060
QY 3061 CGGCTTGTGCTCACCTGTGTGTGCGGAGTGTGAGAGGACAGTGAAGAGAGGTGT 3120
Db 3061 CGGCTTGTGCTCACCTGTGTGTGCGGAGTGTGAGAGGACAGTGAAGAGAGGTGT 3120
QY 3121 CAGGTGTGTGACCCCGGATTCAGAGCTCCCTATGAAACAATCCATGCACTGTGAGAC 3180
Db 3121 CAGGTGTGTGACCCCGGATTCAGAGCTCCCTATGAAACAATCCATGCACTGTGAGAC 3180
QY 3181 ATCAGACAGAGCGCGCTGACCATTTGAGGCTACCTTCTGTGTGTGACACAGAGAG 3240
Db 3181 ATCAGACAGAGCGCGCTGACCATTTGAGGCTACCTTCTGTGTGTGACACAGAGAG 3240
QY 3241 GTTCAAGACGTGTGCGCATGTGGATGGGCTGTGAGAGCGGGGTTCTGTAAAGAG 3300
Db 3241 GTTCAAGACGTGTGCGCATGTGGATGGGCTGTGAGAGCGGGGTTCTGTAAAGAG 3300
QY 3301 CTGAGTGGCCCGGCGCTGCGCAAGGACCTGTGATGACCTTCACTGCGTGTCTGAG 3360
Db 3301 CTGAGTGGCCCGGCGCTGCGCAAGGACCTGTGATGACCTTCACTGCGTGTCTGAG 3360
QY 3361 TTCAAGCACTGACTTCTTCAACAGCAAGAGGCTTTGCAATTTTCAATGATGCA 3420
Db 3361 TTCAAGCACTGACTTCTTCAACAGCAAGAGGCTTTGCAATTTTCAATGATGCA 3420
QY 3421 GCAAGCTGTGCAATGACCTGTGGATCCCGCAATGGAGTGGAGTGTGACAGTTGG 3480
Db 3421 GCAAGCTGTGCAATGACCTGTGGATCCCGCAATGGAGTGGAGTGTGACAGTTGG 3480
QY 3481 GAAGCGGCGCATCTCAAGTGTTCAGAGTGAACCTGAGCTACCGGCTGACAGGAAAGTGA 3540
Db 3481 GAAGCGGCGCATCTCAAGTGTTCAGAGTGAACCTGAGCTACCGGCTGACAGGAAAGTGA 3540
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Db 3541 GAGATCAGCTGTGTGAAGATGAGAACAGGTTCTTGTGGAGCCGACCGCCCAATGC 3600
QY 3601 ATCGCTCCCTGCGGGGAGACCTGACAGAACCATCTGAGAGCATCTCTCAACAAATTC 3660
Db 3601 ATCGCTCCCTGCGGGGAGACCTGACAGAACCATCTGAGAGCATCTCTCAACAAATTC 3660
QY 3661 CCAGAACCTTACCCGCAAGGAGAGTGTGACTGAAAGTGAACGCTCAGCACTAC 3720
Db 3661 CCAGAACCTTACCCGCAAGGAGAGTGTGACTGAAAGTGAACGCTCAGCACTAC 3720
QY 3721 GTCATGCGCTGTGATTTAAATCTTTTAACTGTGAGCCGTGCTATGACTTCTCATATC 3780
Db 3721 GTCATGCGCTGTGATTTAAATCTTTTAACTGTGAGCCGTGCTATGACTTCTCATATC 3780
QY 3781 TACAGCGAGCGGAGCTCTTCAAGCCCTCAATGAAGGCTCTTATGCTCCAGCTCCA 3840
Db 3781 TACAGCGAGCGGAGCTCTTCAAGCCCTCAATGAAGGCTCTTATGCTCCAGCTCCA 3840
QY 3841 GGCAGCAATTTGAAACAGAGCAAGCCTTCTCTGCGCTTCCGAGAGATGCAATCTGTG 3900
Db 3841 GGCAGCAATTTGAAACAGAGCAAGCCTTCTCTGCGCTTCCGAGAGATGCAATCTGTG 3900
QY 3901 AGCAATGCTGCTGTGATTTAATCAAGAAAACCCGCGGAGTCAATGTTTGAATCT 3960
Db 3901 AGCAATGCTGCTGTGATTTAATCAAGAAAACCCGCGGAGTCAATGTTTGAATCT 3960
QY 3961 GGTTCATCAAGAACGAGACAGGAGTGGGTCGACCTGAAAGTGGGCTCTCGGTAC 4020
Db 3961 GGTTCATCAAGAACGAGACAGGAGTGGGTCGACCTGAAAGTGGGCTCTCGGTAC 4020
QY 4021 TACTACTGCAAGGAGGCTAGAGAGTGAAGGCACTTGAACCTGAGCTGTGATCTGGG 4080
Db 4021 TACTACTGCAAGGAGGCTAGAGAGTGAAGGCACTTGAACCTGAGCTGTGATCTGGG 4080
QY 4081 CCGATGAGGAAGCCCGTGTGGAACAATCCCGGCGCACTGTGACAGCCCTGTGGGGA 4140

Db 4081 CCGATGGGAAGCCCGTGTGAACAATCCCGGCGAGTCTGACAGCCCTCTGGGGGA 4140
Qy 4141 CAGTATGTGGGTTTGGACGGAGTGTCTTCTCCCACTACCCCAAGAACTACACAGT 4200
Db 4141 CAGTATGTGGGTTTGGACGGAGTGTCTTCTCCCACTACCCCAAGAACTACACAGT 4200
Qy 4201 GGCAGATCGGCTGTATTTTGTACTGTGCGCAAGAGCTATGTGGTGTGGCGATTG 4260
Db 4201 GGCAGATCGGCTGTATTTTGTACTGTGCGCAAGAGCTATGTGGTGTGGCGATTG 4260
Qy 4261 GCGTCTTTTCAACGCGCCCTCAACGACGTGTGGAGTTTCAACGCGCAACGCGAC 4320
Db 4261 GCGTCTTTTCAACGCGCCCTCAACGACGTGTGGAGTTTCAACGCGCAACGCGAC 4320
Qy 4321 TCGCGGCTCTGAGCTCTCTGTGGGCTCCCATACAGAGATCATCTGCTTGGCCAC 4380
Db 4321 TCGCGGCTCTGAGCTCTCTGTGGGCTCCCATACAGAGATCATCTGCTTGGCCAC 4380
Qy 4381 TCCAAATCAAGTTCTCATTTAGTTCAAGGCGCAAGGCTTGACACGACAGAGCTTCCAC 4440
Db 4381 TCCAAATCAAGTTCTCATTTAGTTCAAGGCGCAAGGCTTGACACGACAGAGCTTCCAC 4440
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Db 4501 CGCTATGCGAAGAGGCTGGGCACTGTTCTCGTGGGGGCAATCGTCCGCTTCAATGC 4560
Qy 4561 AACTCGGCTATCCCTGCGAGGGGTGCGAGATGAGAGTCCCTGTGGGCTTGGGGCC 4620
Db 4561 AACTCGGCTATCCCTGCGAGGGGTGCGAGATGAGAGTCCCTGTGGGCTTGGGGCC 4620
Qy 4621 TTGGCCCAATGATGATCTCAGGCGCCACGTTGTGTGCTGTGGAGGCAACTCACA 4680
Db 4621 TTGGCCCAATGATGATCTCAGGCGCCACGTTGTGTGCTGTGGAGGCAACTCACA 4680
Qy 4681 GAGCGAGAGGCGCAACATCTGTCTCCCTGCTTCCAGAGCGTATCTCAACAGCTTCAAC 4740
Db 4681 GAGCGAGAGGCGCAACATCTGTCTCCCTGCTTCCAGAGCGTATCTCAACAGCTTCAAC 4740
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Db 4741 TGTGTGTGAAGATCGTGTCTCCCGAAGGGCTGTGCTTCCAGATCCAAAGTTGTCAATTT 4800
Qy 4801 GTGACAGAGAGAGCTGGAGCTGCTGAGAGTATTTGATGTGCAATACCTGTAACTGTAACT 4860
Db 4801 GTGACAGAGAGAGCTGGAGCTGCTGAGAGTATTTGATGTGCAATACCTGTAACTGTAACT 4860
Qy 4861 ATGCTGGGAGATTTCTCAGGAACAACCGTCTGCTTCTGAACAGCACTTCAACAG 4920
Db 4861 ATGCTGGGAGATTTCTCAGGAACAACCGTCTGCTTCTGAACAGCACTTCAACAG 4920
Qy 4921 CTCTACCTTCAATTTCTACTCAGATATCAGGCTATCTGCACTGCTTCACTTGGATAC 4980
Db 4921 CTCTACCTTCAATTTCTACTCAGATATCAGGCTATCTGCACTGCTTCACTTGGATAC 4980
Qy 4981 AAAAGGTTGGGCTGAGAGCTGTTGCGGAACCTGTGCGCAAGTAAAGGAGTAAAGT 5040
Db 4981 AAAAGGTTGGGCTGAGAGCTGTTGCGGAACCTGTGCGCAAGTAAAGGAGTAAAGT 5040
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Db 5041 GGGGAGGCTACTTGTGTGAATGTGTGTCTTTTCAAGTGTGAAGCGGGATATGCGCTC 5100
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Db 5101 CAGGGGCAAGCCCACTCTCTGTGATGCTGCGGAACAGTGGGAGTGAATCTACCTCTCT 5160
Qy 5161 CCACTCTGTATTTGACAGTGTGGGGGAACGTGAGAGATGAGGGGGTGTCTGAGC 5220
Db 5161 CCACTCTGTATTTGACAGTGTGGGGGAACGTGAGAGATGAGGGGGTGTCTGAGC 5220
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Db 5221 CCGGCTTCCAGGCAACTACCCCACTAATGAGATTTGCTTCTGGAAAAATGACATGCCC 5280
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Db 5281 GTGGGCTTTGAGAGCTCAGATCCAGTCTCTGAATCTTCTCAACGAGCGCAACAGACTAC 5340
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Db 5341 ATGAAATCCGGAATGAGGCTTATGAGACCAAGCGCATATGGAAGATTCACTGGAAGC 5400
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Db 5401 GAGCTTCCAAAGCTCTCTCTTCCAGTCCCAAGAACCAAGCTGTATTTTCCACAGCAG 5460
Qy 5461 CACTCCAGATGAGGCGAGGATTCAGAGTATCAGGCTATGAACTTCAAGAGTGC 5520
Db 5461 CACTCCAGATGAGGCGAGGATTCAGAGTATCAGGCTATGAACTTCAAGAGTGC 5520
Qy 5521 CCAGACCAAGAGCCCTTTGCGCAATGSCATTTGTAGGGGAGCTGCTACAACTGGGACAA 5580
Db 5521 CCAGACCAAGAGCCCTTTGCGCAATGSCATTTGTAGGGGAGCTGCTACAACTGGGACAA 5580
Qy 5581 TCAGTACCTTGAAGTCTCTCCGGGGTATCAATTGACTGGCCACCTGTCTCACTGT 5640
Db 5581 TCAGTACCTTGAAGTCTCTCCGGGGTATCAATTGACTGGCCACCTGTCTCACTGT 5640
Qy 5641 CAACATGAGCAACCAAGGAACTGGAGCAACCCCTGCGCAAGGTGAAGTCCCTTGGG 5700
Db 5641 CAACATGAGCAACCAAGGAACTGGAGCAACCCCTGCGCAAGGTGAAGTCCCTTGGG 5700
Qy 5701 GGGAAATCACTTTTCAACGAGCACTGTACTCCCGGGGTTCTTACGCCGTACTCC 5760
Db 5701 GGGAAATCACTTTTCAACGAGCACTGTACTCCCGGGGTTCTTACGCCGTACTCC 5760
Qy 5761 AGCTCCAGAGAGCTGTCTGAGTATCAGCGTCCATTTGGCCATGCGGCTTCCAC 5820
Db 5761 AGCTCCAGAGAGCTGTCTGAGTATCAGCGTCCATTTGGCCATGCGGCTTCCAC 5820
Qy 5821 CTGAGCTGTGAGACAGAGCCCTGAGAGATTTTATCACAATCTGGAGTGGGCCACAG 5880
Db 5821 CTGAGCTGTGAGACAGAGCCCTGAGAGATTTTATCACAATCTGGAGTGGGCCACAG 5880
Qy 5881 CAAACAGACCAAGGCTGCGGCTTCAACCGGAGGATGAGCAAGTGCAGAGT 5940
Db 5881 CAAACAGACCAAGGCTGCGGCTTCAACCGGAGGATGAGCAAGTGCAGAGT 5940
Qy 5941 TCATCCACCAAGGCTCTGCTCAAGTTTCAACCGTATGACAGCCACAGGGGAGATCTTCCG 6000
Db 5941 TCATCCACCAAGGCTCTGCTCAAGTTTCAACCGTATGACAGCCACAGGGGAGATCTTCCG 6000
Qy 6001 ATAGCTTTTCTCGCTTATCCACTCAACAATGCGCTCTCCCAACATCTCCCAAGCC 6060
Db 6001 ATAGCTTTTCTCGCTTATCCACTCAACAATGCGCTCTCCCAACATCTCCCAAGCC 6060
Qy 6061 GAAAGCTGACAGAGATGAAGATTAATTAAGTGAATCTGACCTTCAAGATCTCTC 6120
Db 6061 GAAAGCTGACAGAGATGAAGATTAATTAAGTGAATCTGACCTTCAAGATCTCTC 6120
Qy 6121 CCGGCTTTTACCTTATGAGGAAATGAATTTCTGACCTGCAAACTTGGAACTTACCTG 6180
Db 6121 CCGGCTTTTACCTTATGAGGAAATGAATTTCTGACCTGCAAACTTGGAACTTACCTG 6180
Qy 6181 TTTGAAGAACCAACCCCGATGATGAGTGCATGTCACCAAAATGAGCTTCAAGAC 6240
Db 6181 TTTGAAGAACCAACCCCGATGATGAGTGCATGTCACCAAAATGAGCTTCAAGAC 6240
Qy 6241 TCCACAGAGGATCTCTGAGCCAGAGCTACCTTGAAGTATCCCAAGTTCAGACTGC 6300
Db 6241 TCCACAGAGGATCTCTGAGCCAGAGCTACCTTGAAGTATCCCAAGTTCAGACTGC 6300
Qy 6300 TCCACAGAGGATCTCTGAGCCAGAGCTACCTTGAAGTATCCCAAGTTCAGACTGC 6300
Db 6300 TCCACAGAGGATCTCTGAGCCAGAGCTACCTTGAAGTATCCCAAGTTCAGACTGC 6300

XX 22-AUG-2002.
 XX 10-DEC-2001; 2001WO-US048369.
 XX 08-DEC-2000; 2000US-0254329P.
 PR 14-DEC-2000; 2000US-0255648P.
 PR 15-MAY-2001; 2001US-0291037P.
 PR 08-JUN-2001; 2001US-0292173P.
 PR 08-JUN-2001; 2001US-0309258P.
 PR 29-AUG-2001; 2001US-0315639P.
 PR 01-OCT-2001; 2001US-0326393P.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Alsbrook JP, Anderson DW, Burgess CE, Boldog FL, Casman SJ,
 PI Colman SD, Edinger SR, Ellerman K, Gerlach V, Gorman U, Grosse WM,
 PI Guo X, Herzmann JL, Kekuda R, Lepley DW, Li L, Macdougall JR, -
 PI Millet I, Pena CE, Peyman JA, Raselli L, Rieger DK, Shinkels RA,
 PI Smithson G, Szytek KA, Stone DJ, Tchernev VT, Vernet CM, Voss EZ,
 PI Zernhusen BD, Zhong H, Zhong M;
 DR MPI; 2002-643486/69.
 XX P-PSDB; ABG79169.
 XX
 PT New NOVX polypeptides and polynucleotides useful for treating or
 PT preventing e.g. neurodegenerative diseases, neurological disorders,
 PT cardiovascular diseases, muscular diseases and disorders, or
 PT immunological diseases.
 XX
 XX Claim 9; Page 14-16; 299pp; English.
 XX
 CC The present invention relates to new NOVX polypeptides. The polypeptides,
 CC polynucleotides and antibodies are useful in the manufacture of a
 CC medicament for treating or preventing neurodegenerative diseases (e.g.
 CC Alzheimer's disease, Parkinson's disease, or Huntington's disease),
 CC neurological disorders (e.g. anxiety, schizophrenia, manic depression or
 CC mental retardation), cardiovascular disease (e.g. acute heart failure,
 CC angina pectoris or myocardial infarction), muscular diseases and
 CC disorders, retinal diseases (including those involving photoreception,
 CC deafness and keratinisation disorders), cancer (e.g. ovarian cancer or
 CC melanoma), immunological disorders, inflammatory and immune diseases,
 CC bacterial, fungal, protozoal and viral infections, and reproductive
 CC system disorders. The proteins of the invention may be used to screen
 CC drugs or compounds that modulate the NOVX protein activity or expression,
 CC as well as to treat disorders characterised by insufficient or excessive
 CC production of NOVX protein or protein forms that have decreased or
 CC aberrant activity compared to NOVX wild type protein, such as diabetes,
 CC obesity, metabolic disturbances associated with obesity, anorexia and
 CC wasting disorders associated with chronic diseases and various cancers,
 CC infectious diseases and various dyslipidaemias. The nucleic acid
 CC sequences of the invention may be used in chromosome mapping, identifying
 CC an individual from minute biological samples (tissue typing), and in
 CC forensic identification of a biological sample. The present nucleic acid
 CC sequence encodes a NOVX protein of the invention
 XX
 XX Sequence 8010 BP; 1720 A; 2412 C; 2140 G; 1738 T; 0 U; 0 Other;
 SQ
 Query Match 75.1%; Score 7614.8; DB 6; Length 8010;
 Best Local Similarity 97.8%; Pred. No. 0;
 Matches 7823; Conservative 0; Mismatches 2; Indels 177; Gaps 3;

QY 181 GTGTTAACTCAGGTGTTGTTGTTCCAAAGGACATAATATGTTCCAGACCTCGCATACCC 240
 DB 181 GTGTTAACTCAGGTGTTGTTGTTCCAAAGGACATAATATGTTCCAGACCTCGCATACCC 240
 QY 241 GAAAGGGGCAAAAGACTAGAGCTCGATTTCAGTTAGATTCAGCTCCAGTTCACTTCG 300
 DB 241 GAAAGGGGCAAAAGACTAGAGCTCGATTTCAGTTAGATTCAGCTCCAGTTCACTTCG 300
 QY 301 AACGAGGGCTATGACTCGAAGGGTCCAAAGCGGATCACTGTATGAAAGTGAAGCGACATG 360
 DB 301 AACGAGGGCTATGACTCGAAGGGTCCAAAGCGGATCACTGTATGAAAGTGAAGCGACATG 360
 QY 361 TTTGCGGCTGAGGCGCAACAAGCGGCTGCGGAGCCCGCATGTGTATGCTCCACTT 420
 DB 361 TTTGCGGCTGAGGCGCAACAAGCGGCTGCGGAGCCCGCATGTGTATGCTCCACTT 420
 QY 421 CGAGGCGCTCGGCGCATCATCTCCCAATTTCCCATTCAGTATGACAAATGCA 480
 DB 421 CGAGGCGCTCGGCGCATCATCTCCCAATTTCCCATTCAGTATGACAAATGCA 480
 QY 481 CACTGTGTGATCATCAAGACATCAACCCCTCCAGGTGATCAAGCTCGCTTTGAG 540
 DB 481 CACTGTGTGATCATCAAGACATCAACCCCTCCAGGTGATCAAGCTCGCTTTGAG 540
 QY 541 GAGTTGATTTGAGAGGGGCTATGACACCTCGACGGTGTGATGTTGTCAGATGCG 600
 DB 541 GAGTTGATTTGAGAGGGGCTATGACACCTCGACGGTGTGATGTTGTCAGATGCG 600
 QY 601 GACCAAGACAGATTCTCTACATGTCTCAAAAATGCTGACAGTACAGCCCTCACACCCA 660
 DB 601 GACCAAGACAGATTCTCTACATGTCTCAAAAATGCTGACAGTACAGCCCTCACACCCA 660
 QY 661 GGCTTCGATCCAGAGAGCATGTCTGAGGACATCTGAGGAGCAAAATGACTGTACTT 720
 DB 661 GGCTTCGATCCAGAGAGCATGTCTGAGGACATCTGAGGAGCAAAATGACTGTACTT 720
 QY 721 GAGATTTGTCGATCACTTTCAGATTGACATGCAAGTCAAGTTCAGTGAAGTCTCCA 780
 DB 721 GAGATTTGTCGATCACTTTCAGATTGACATGCAAGTCAAGTTCAGTGAAGTCTCCA 780
 QY 781 AAGACTTCTAATGCTGTGGAACCTTGTGCTCGGAGAGAGATCGAGAGGGCAGTTGC 840
 DB 781 AAGACTTCTAATGCTGTGGAACCTTGTGCTCGGAGAGAGATCGAGAGGGCAGTTGC 840
 QY 841 GGTGACCTTGACATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 900
 DB 841 GGTGACCTTGACATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 900
 QY 901 ACACTAAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 960
 DB 901 ACACTAAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 960
 QY 961 CAAAAGATTAACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020
 DB 961 CAAAAGATTAACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020
 QY 1021 TTCACAGCCCGTCTGAGGTTGCTGTCTCTCCCAATTAACCAAGAGATTAAGCAACAC 1080
 DB 1021 TTCACAGCCCGTCTGAGGTTGCTGTCTCTCCCAATTAACCAAGAGATTAAGCAACAC 1080
 QY 1081 CTCACATGTTGTTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 1140
 DB 1081 CTCACATGTTGTTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 1140
 QY 1141 GACATTGAGTGAAGCTCAAGTTTATTTCTGATCATCAAGATGAGGACACCGCCGAG 1200
 DB 1141 GACATTGAGTGAAGCTCAAGTTTATTTCTGATCATCAAGATGAGGACACCGCCGAG 1200
 QY 1201 GGGCCCGTCTGAGGACATTTCTCAGAAACCAAGCTTCCCTCTCATCAACAGCACTGAC 1260
 DB 1201 GGGCCCGTCTGAGGACATTTCTCAGAAACCAAGCTTCCCTCTCATCAACAGCACTGAC 1260

QY 1261 CAGTGGCCGCTCTCGAGTTCAGACTGACCACTCCACAGGGAGAGGGCTTCAACATC 1320
DB 1261 CAGTGGCCGCTCTCGAGTTCAGACTGACCACTCCACAGGGAGAGGGCTTCAACATC 1320
QY 1321 ACTTTTACCACTTCCGACCAACAGAGTGGCCGGATCTGGCGTTCCAGTAAATGGCAA 1380
DB 1321 ACTTTTACCACTTCCGACCAACAGAGTGGCCGGATCTGGCGTTCCAGTAAATGGCAA 1380
QY 1381 CGGTTTGGGGAGACGCTCCAGCTGGGAGCTGCACTCCCTCTCTGTGATGAAGGCTTC 1440
DB 1381 CGGTTTGGGGAGACGCTCCAGCTGGGAGCTGCACTCCCTCTCTGTGATGAAGGCTTC 1440
QY 1441 CTGGGACTCAGGGCTCAGAGACCACTCCTGCTCTGAAGAGGGAGCGTGTCTGG 1500
DB 1441 CTGGGACTCAGGGCTCAGAGACCACTCCTGCTCTGAAGAGGGAGCGTGTCTGG 1500
QY 1501 AACAGCGCTGTGCTGGGTGTGAAGTCCCTGTGTGTGACCTGACTTGGCCAGCGGC 1560
DB 1501 AACAGCGCTGTGCTGGGTGTGAAGTCCCTGTGTGTGACCTGACTTGGCCAGCGGC 1560
QY 1561 ACCATCTCTCTCCGGGCTGGGCTGGCTCTACAGAGAGTCCCTGAGCTGTGCTGGGTT 1620
DB 1561 ACCATCTCTCTCCGGGCTGGGCTGGCTCTACAGAGAGTCCCTGAGCTGTGCTGGGTT 1620
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DB 1621 ATTGAGGCCAGCCAGGCTTACCCTCAATAATCACTTCGACAGATTCAAAACGAGGTC 1680
QY 1681 AACTATGACACCTCTGGAAGTACGGATGGGCGGACTTACTCAGCGCCCTTGATCGGGTT 1740
DB 1681 AACTATGACACCTCTGGAAGTACGGATGGGCGGACTTACTCAGCGCCCTTGATCGGGTT 1740
QY 1741 TACGAGGGAGCCAGGTTCCCGAGTTCCTCATCAGACAGGACACTACCTCACTCTCTC 1800
DB 1741 TACGAGGGAGCCAGGTTCCCGAGTTCCTCATCAGACAGGACACTACCTCACTCTCTC 1800
QY 1801 TTCTCTACCGACAGAGTCACTCTGACATCGGCTTCAGCTCCGCTATGAGACTAACA 1860
DB 1801 TTCTCTACCGACAGAGTCACTCTGACATCGGCTTCAGCTCCGCTATGAGACTAACA 1860
QY 1861 CTGCACTCAGACCACTGTCTGGATCCAGAAATCCAGTAAATGACAGGCTATGGGAAT 1920
DB 1861 CTGCACTCAGACCACTGTCTGGATCCAGAAATCCAGTAAATGACAGGCTATGGGAAT 1920
QY 1921 GACTTCTAGTGGGCGCGCTGGTGAACCTTCAGCTGAGCTCGGGGCTACACATTAAAGTGC 1980
DB 1921 GACTTCTAGTGGGCGCGCTGGTGAACCTTCAGCTGAGCTCGGGGCTACACATTAAAGTGC 1980
QY 1981 GGGGAGCCCTCTGAGAGTGTAGGCCCACTTCAGTGGAGCGGGCCCTGCGCAGTTGTGA 2040
DB 1981 GGGGAGCCCTCTGAGAGTGTAGGCCCACTTCAGTGGAGCGGGCCCTGCGCAGTTGTGA 2040
QY 2041 GCTCTCTGTGTGGCTTCACTTAAGGCTCAGATGGGACCATCTTGTCCGAGGGTTCCCT 2100
DB 2041 GCTCTCTGTGTGGCTTCACTTAAGGCTCAGATGGGACCATCTTGTCCGAGGGTTCCCT 2100
QY 2101 GACTTCTAGCCCAACAACTTGAAGTGCACCTGATTAATGAACATCTCATGGAGAGGT 2160
DB 2101 GACTTCTAGCCCAACAACTTGAAGTGCACCTGATTAATGAACATCTCATGGAGAGGT 2160
QY 2161 GTGTTCTTCACTTCCACACTTTCACCTGAAAAGTGGCCATGACTACTCTCTCATCT 2220
DB 2161 GTGTTCTTCACTTCCACACTTTCACCTGAAAAGTGGCCATGACTACTCTCTCATCT 2220
QY 2221 GAGGAGCGGAGCTTCAACCAAGCCCTGAGGCACTTAATGATCTGGCTGCACTGCC 2280
DB 2221 GAGGAGCGGAGCTTCAACCAAGCCCTGAGGCACTTAATGATCTGGCTGCACTGCC 2280
QY 2281 ATCAGAGCTGGGCTCTATGGCAACTTCACTGCGCAGGTCGGCTATCTGATTTCTCC 2340
DB 2281 ATCAGAGCTGGGCTCTATGGCAACTTCACTGCGCAGGTCGGCTATCTGATTTCTCC 2340
QY 2341 ATGTGATATGAAGATTCAACATCACTTCTCAGAGTACGACTTGGAGCCCTGTGGAG 2400

DB 2341 ATGTGATATGAAGATTCAACATCACTTCTCAGAGTACGACTTGGAGCCCTGTGGAG 2400
QY 2401 CCCGAGGTCCTCAAGCTTACAGCATCCGGAAGGGCTTGCAGTTTGGCTGGCGACCTTG 2460
DB 2401 CCCGAGGTCCTCAAGCTTACAGCATCCGGAAGGGCTTGCAGTTTGGCTGGCGACCTTG 2460
QY 2461 AACTTCTCTGCTTCCCGGGGTAACGCTGGAAGGCAACCGGCCGATCACTGCTGGGG 2520
DB 2461 AACTTCTCTGCTTCCCGGGGTAACGCTGGAAGGCAACCGGCCGATCACTGCTGGGG 2520
QY 2521 GGCAGACCGCGCTGTGAGCTCGCTCTGCAAGAGTGTGTGCTGAGTGTGGAAATCA 2580
DB 2521 GGCAGACCGCGCTGTGAGCTCGCTCTGCAAGAGTGTGTGCTGAGTGTGGAAATCA 2580
QY 2581 GTCAAGGCACTCAGGGTACTTGTGCTGCTCCCACTTCTCTGTAATCAATTAACAT 2640
DB 2581 GTCAAGGCACTCAGGGTACTTGTGCTGCTCCCACTTCTCTGTAATCAATTAACAT 2640
QY 2641 CATGATGATCATCTCATCATCAGACCCAGGAGGGAATTCACTGTAAGGCCAGG 2700
DB 2641 CATGATGATCATCTCATCATCAGACCCAGGAGGGAATTCACTGTAAGGCCAGG 2700
QY 2701 GCATTGCAACTCTCCGAGAGAGATGCTCTCAAGGTTTATGATGGCAACAACTCCGCC 2760
DB 2701 GCATTGCAACTCTCCGAGAGAGATGCTCTCAAGGTTTATGATGGCAACAACTCCGCC 2760
QY 2761 CGTTTGTGGGAGTTTATGAGCACTTCTGATGATGAGGGGTGACTTTGAACAGCAATCC 2820
DB 2761 CGTTTGTGGGAGTTTATGAGCACTTCTGATGATGAGGGGTGACTTTGAACAGCAATCC 2820
QY 2821 AGCAGCTGTGGCTTGAATTTTATCATCATGATGCTGAAAAACACAGAGAGGCTTTGAATG 2880
DB 2821 AGCAGCTGTGGCTTGAATTTTATCATCATGATGCTGAAAAACACAGAGAGGCTTTGAATG 2880
QY 2881 CACTTTTCCAGCTTTGAATCTCATCAATGTTGAGAGACCCAGAACTTTGGCTAC 2940
DB 2881 CACTTTTCCAGCTTTGAATCTCATCAATGTTGAGAGACCCAGAACTTTGGCTAC 2940
QY 2941 AAGGTTATGATGAAGTCACTTTTGCAGAGAGCTCCGTGCTCTTCACTGTGACCTTGA 3000
DB 2941 AAGGTTATGATGAAGTCACTTTTGCAGAGAGCTCCGTGCTCTTCACTGTGACCTTGA 3000
QY 3001 TACAGCCTGCGGGGTAGTGAAGAGCTGCTGTGTGATGATGAGAGCGCGGACCTGGAG 3060
DB 3001 TACAGCCTGCGGGGTAGTGAAGAGCTGCTGTGTGATGATGAGAGCGCGGACCTGGAG 3060
QY 3061 CGGCTCTGCCACCTGTGTGCGAGTGTGAGAGGGAACATGAGAGAGAGGCTGTGGGG 3120
DB 3061 CGGCTCTGCCACCTGTGTGCGAGTGTGAGAGGGAACATGAGAGAGAGGCTGTGGGG 3120
QY 3121 CAGGTGCTGTACCCCGGGGTATCCAGCTCCCTATGAACAACTGATCTGAGACC 3180
DB 3121 CAGGTGCTGTACCCCGGGGTATCCAGCTCCCTATGAACAACTGATCTGAGACC 3180
QY 3181 ATCGAAGAGAGGCGGCTGACCACTTGGGCTACACTTCTGATTTTGAACAGAGAG 3240
DB 3181 ATCGAAGAGAGGCGGCTGACCACTTGGGCTACACTTCTGATTTTGAACAGAGAG 3240
QY 3241 GTTCAAGAGCTGTGCGCATCTGGAGTGGGCTGTGAGAGAGCGGGCTTCTGAAGAG 3300
DB 3241 GTTCAAGAGCTGTGCGCATCTGGAGTGGGCTGTGAGAGAGCGGGCTTCTGAAGAG 3300
QY 3301 CTGAGTGGCCCGGCTGCGCCAGAGAGCTGATGACCTTCAACTGGTGTCTGGAG 3360
DB 3301 CTGAGTGGCCCGGCTGCGCCAGAGAGCTGATGACCTTCAACTGGTGTCTGGAG 3360
QY 3361 TTCAAGCACTGACTTCTTCAACAGAGAGAGGCTTGTCCATTTTCAAGTGTCCACA 3420
DB 3361 TTCAAGCACTGACTTCTTCAACAGAGAGAGGCTTGTCCATTTTCAAGTGTCCACA 3420
QY 3421 GCAAGCTCTGCAATGACCTGGGATCCGCAAGATGGAGTGGAGTGTGACAGTTGG 3480

Dh 3421 GCAACGTCCTGCAATGACCCCTGGGAATCCGACAGAAATGGAGTGGAGTGGATGCAAGTTGG 3480
Qy 3481 GAAGCGGCGGCACTCCAAGTGTTCAGTGTGACCTTGCGTGGCTGACGGGAGTGGCA 3540
Dh 3481 GAAGCGGCGGCACTCCAAGTGTTCAGTGTGACCTTGCGTGGCTGACGGGAGTGGCA 3540
Qy 3541 GAAGTCACTGTGTGAAAGATCGAAGAACAGGTTCTTCTGCGAGCCGACGCCCAAGATGC 3600
Dh 3541 GAAGTCACTGTGTGAAAGATCGAAGAACAGGTTCTTCTGCGAGCCGACGCCCAAGATGC 3600
Qy 3601 ATGCTCTCTGCGGGGGAGACTGACAGAGCACTCTGAGATCATCTCTTCAACCAATTAAC 3660
Dh 3601 ATGCTCTCTGCGGGGGAGACTGACAGAGCACTCTGAGATCATCTCTTCAACCAATTAAC 3660
Qy 3661 CCAGAACCCCTACCCGCGGCGGCAAGAGTGTGACCTGGAAGTGAACCGCTTCAACGACTAC 3720
Dh 3661 CCAGAACCCCTACCCGCGGCGGCAAGAGTGTGACCTGGAAGTGAACCGCTTCAACGACTAC 3720
Qy 3721 GTTCATCGCCCTGTGATTTAAACATCTTTAACTTGAGCTTGAGCTTATGATTC 3780
Dh 3721 GTTCATCGCCCTGTGATTTAAACATCTTTAACTTGAGCTTGAGCTTATGATTC 3780
Qy 3781 TACGACGGAAGGGAAGCTCTCTGAGCCCTCTCATAGAAAGCTTCTATGAGCTTCCAGCTTCCA 3840
Dh 3781 TACGACGGAAGGGAAGCTCTCTGAGCCCTCTCATAGAAAGCTTCTATGAGCTTCCAGCTTCCA 3840
Qy 3841 GGGCGGATTTGAAGGAGGAGGCAACGCTCTTCTGCGCTTCCGCGGAGCTGATCTGTC 3900
Dh 3841 GGGCGGATTTGAAGGAGGAGGCAACGCTCTTCTGCGCTTCCGCGGAGCTGATCTGTC 3900
Qy 3901 AGCAATGTGGCTTCTGATTTAACTTTAACTTGAGCTTGAGCTTATGATTC 3960
Dh 3901 AGCAATGTGGCTTCTGATTTAACTTTAACTTGAGCTTGAGCTTATGATTC 3960
Qy 3961 GGTTCATCAAGAACGAGCAACGAGGTGGGGTCCGACCTGAAAGCTGGGCTCTCCGTCAC 4020
Dh 3961 GGTTCATCAAGAACGAGCAACGAGGTGGGGTCCGACCTGAAAGCTGGGCTCTCCGTCAC 4020
Qy 4021 TACTATGCGACCGGGGCTTACGAAATTTGAGGAGCACTTCCGACCTGAGCTGATCTGAGG 4080
Dh 4021 TACTATGCGACCGGGGCTTACGAAATTTGAGGAGCACTTCCGACCTGAGCTGATCTGAGG 4080
Qy 4081 CCTGATGGGAAGCCGCTGTGGAACAATCCCGGCGAGCTGACAGAGCCCTTGTGGGGA 4140
Dh 4081 CCTGATGGGAAGCCGCTGTGGAACAATCCCGGCGAGCTGACAGAGCCCTTGTGGGGA 4140
Qy 4141 CAGTATGTGGGTTCCGACGGAAGTGTCTTGTCCCACTAATCCCGGAGACTGACAGT 4200
Dh 4141 CAGTATGTGGGTTCCGACGGAAGTGTCTTGTCCCACTAATCCCGGAGACTGACAGT 4200
Qy 4201 GGAAGATCTGCTTGTATTTTGTACTGTCTCCCAAGACTATGTGTGTGGCCAGTTTC 4260
Dh 4201 GGAAGATCTGCTTGTATTTTGTACTGTCTCCCAAGACTATGTGTGTGGCCAGTTTC 4260
Qy 4261 GCTTCTTTTCAACGCGCCCTCAAGAGTGTGAGGTTTCCAGAGGAGCAACGAGCAGC 4320
Dh 4261 GCTTCTTTTCAACGCGCCCTCAAGAGTGTGAGGTTTCCAGAGGAGCAACGAGCAGC 4320
Qy 4321 TGGCGGCTCTCAAGCTCTCTGCGGCTCCCATACAGAGATCACTGCGCTTGGCCAGC 4380
Dh 4321 TGGCGGCTCTCAAGCTCTCTGCGGCTCCCATACAGAGATCACTGCGCTTGGCCAGC 4380
Qy 4381 TCCAAATCAAGTTCTCTTAAGTTCAAGGCGCAAGGCTCTGACACAGAGGCTTTCAC 4440
Dh 4381 TCCAAATCAAGTTCTCTTAAGTTCAAGGCGCAAGGCTCTGACACAGAGGCTTTCAC 4440
Qy 4441 TTTGTATCAACAGCGGTTCTTGAACGAGGCGCAACGAGTGAAGTCTGTGCGGGAACCC 4500
Dh 4441 TTTGTATCAACAGCGGTTCTTGAACGAGGCGCAACGAGTGAAGTCTGTGCGGGAACCC 4500
Qy 4501 CGGTATGGAAGAGGCTGGGCAATGATCTTCTCGGTGGGGCACTGCTCGCTTCCGAATGC 4560
Dh 4501 CGGTATGGAAGAGGCTGGGCAATGATCTTCTCGGTGGGGCACTGCTCGCTTCCGAATGC 4560

Qy 4561 AACTCCGCTATATCCCTGACGAGGAGTCCGACAGATGAGTCCCTGCTGCTGGGAGC 4620
Dh 4561 AACTCCGCTATATCCCTGACGAGGAGTCCGACAGATGAGTCCCTGCTGCTGGGAGC 4620
Qy 4621 TTGGCCCAATGGAATGTCTCAGGCGCCACGCTGTGTGTGTCGAGGAGCACTTCA 4680
Dh 4621 TTGGCCCAATGGAATGTCTCAGGCGCCACGCTGTGTGTGTCGAGGAGCACTTCA 4680
Qy 4681 GAGCGGAGGAGGCACTTCTGTCTCTGCTTCCGAGGCTTCACTCAAGCTTCAAC 4740
Dh 4681 GAGCGGAGGAGGCACTTCTGTCTCTGCTTCCGAGGCTTCACTCAAGCTTCAAC 4740
Qy 4741 TGTGTGTGAAGATGTGTGTGTCGAGGAGGCTGAGTCAAGTCCAGTGTGCACTTT 4800
Dh 4741 TGTGTGTGAAGATGTGTGTGTCGAGGAGGCTGAGTCAAGTTCAGTGTGCACTTT 4800
Qy 4801 GTGACAGAGCAGAACCTGAGGAGCTGCTGGAAGATTTGATGTGTGCAATTAACATGTAAAC 4860
Dh 4801 GTGACAGAGCAGAACCTGAGGAGCTGCTGGAAGATTTGATGTGTGCAATTAACATGTAAAC 4860
Qy 4861 ATGCTGGGAGTTTCTCAGGAGCAACGCTGCTGCTTCTGTAACGACCTTCAAC 4920
Dh 4861 ATGCTGGGAGTTTCTCAGGAGCAACGCTGCTGCTTCTGTAACGACCTTCAAC 4920
Qy 4921 CTCTACCTTCAATTTCTACCTCAGATATCAGGATATGACGCTGCTTCACTTGAAGTAC 4980
Dh 4921 CTCTACCTTCAATTTCTACCTCAGATATCAGGATATGACGCTGCTTCACTTGAAGTAC 4980
Qy 4981 AAAACGGTGGGCTGAGAGTGTCCGGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5040
Dh 4981 AAAACGGTGGGCTGAGAGTGTCCGGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5040
Qy 5041 GGGGAGCGCTACTTGTGTATGATGTGTGTCTTTTCAAGTGTGAGCCGAGATATGCCCTTC 5100
Dh 5041 GGGGAGCGCTACTTGTGTATGATGTGTGTCTTTTCAAGTGTGAGCCGAGATATGCCCTTC 5100
Qy 5101 CAGGGGCAAGGCCCACTCTCTGCAATGCTCCGGAACGCTCCGAGAGTGAAGTCACTCCCTCT 5160
Dh 5101 CAGGGGCAAGGCCCACTCTCTGCAATGCTCCGGAACGCTCCGAGAGTGAAGTCACTCCCTCT 5160
Qy 5161 CCACTCTGATTTGCAAGTGTGGGAGGAGAGTGAAGGAGGAGTGAAGTGAAGTGAAGTGAAG 5220
Dh 5161 CCACTCTGATTTGCAAGTGTGGGAGGAGAGTGAAGGAGGAGTGAAGTGAAGTGAAGTGAAG 5220
Qy 5221 CCGGCTTCCAGGCACTAATCCCAAGTAACTGAGCTGCTCTGAAAAATGACATGCTCC 5280
Dh 5221 CCGGCTTCCAGGCACTAATCCCAAGTAACTGAGCTGCTCTGAAAAATGACATGCTCC 5280
Qy 5281 GTGGGCTTTGAGCTCAATCCAGTTCCTGAACTTCTCCAGGAGCCCAACCAAGCTAC 5340
Dh 5281 GTGGGCTTTGAGCTCAATCCAGTTCCTGAACTTCTCCAGGAGCCCAACCAAGCTAC 5340
Qy 5341 ATGAAATCCGGAATGAGCCCTATGAGACGAGCCGATGAGGAGATTCAGTGAAGC 5400
Dh 5341 ATGAAATCCGGAATGAGCCCTATGAGACGAGCCGATGAGGAGATTCAGTGAAGC 5400
Qy 5401 GAGCTTCAAGCTCCTCTCTTCCAGCTCCAGAGCAACCGTGTATTTTCCAGCAGC 5460
Dh 5401 GAGCTTCAAGCTCCTCTCTTCCAGCTCCAGAGCAACCGTGTATTTTCCAGCAGC 5460
Qy 5461 GAGCTTCAAGCTCCTCTCTTCCAGCTCCAGAGCAACCGTGTATTTTCCAGCAGC 5520
Dh 5461 GAGCTTCAAGCTCCTCTCTTCCAGCTCCAGAGCAACCGTGTATTTTCCAGCAGC 5520
Qy 5521 CCAGACCCAGAGCCCTTGTGCAATGAGGAGGAGTGAAGGAGGAGTGAAGGAGGAGTGAAG 5580
Dh 5521 CCAGACCCAGAGCCCTTGTGCAATGAGGAGGAGTGAAGGAGGAGTGAAGGAGGAGTGAAG 5580
Qy 5581 TCAGTGACCTTGAAGTCTCCCGGGATATCAATTAAGTGAAGTGAAGTGAAGTGAAGTGAAG 5640
Dh 5581 TCAGTGACCTTGAAGTCTCCCGGGATATCAATTAAGTGAAGTGAAGTGAAGTGAAGTGAAG 5640

OY	5641	CAACATGGCACCAACCGGAACCTGGGAGCACACCCCGCGCCCAAGTGTGAAGTCCCTGTGGGC	5700
Db	5641	CAACATGGCACCAACCGGAACCTGGGAGCACACCCCGCGCCCAAGTGTGAAGTCCCTGTGGGC	5700
OY	5701	GGGAACATCACTTCTTCCACGGCACGTGTACTCCCGGGGTTCCCTAGGCCGTACTCC	5760
Db	5701	GGGAACATCACTTCTTCCACGGCACGTGTACTCCCGGGGTTCCCTAGGCCGTACTCC	5760
OY	5761	AGCTCCCAAGACCTGTGTCTGGGTGATCACCGTGCCCATTTGGCCATTTGGCCTCAAC	5820
Db	5761	AGCTCCCAAGACCTGTGTCTGGGTGATCACCGTGCCCATTTGGCCTCAAC	5820
OY	5821	CTCAGCCCTGCGACAGACAGCCCTCTGGAATTTTCATCACATCTGGGAATGGGCCACAG	5880
Db	5821	CTCAGCCCTGCGACAGACAGCCCTCTGGAATTTTCATCACATCTGGGAATGGGCCACAG	5880
OY	5881	CAAAACGACACACCGCTCGGGCTCTTCCACCCCGAGCATGGCCAAAGAAAACAGTGCAGAGT	5940
Db	5881	CAAAACGACACACCGCTCGGGCTCTTCCACCCCGAGCATGGCCAAAGAAAACAGTGCAGAGT	5940
OY	5941	TCATTCACACAGGTCTGTCTCAAGTTCCACCGTGATGCAGCCACAGGGGGGATCTTGCC	6000
Db	5941	TCATTCACACAGGTCTGTCTCAAGTTCCACCGTGATGCAGCCACAGGGGGGATCTTGCC	6000
OY	6001	ATAGCTTCTCGGTTATCCACTCAACCAATAGCCCTCTCCACATCTCCCAAGGCC	6060
Db	6001	ATAGCTTCTCGGTTATCCACTCAACCAATAGCCCTCTCCACATCTCTCCCAAGGCC	6060
OY	6061	GAAGTGTCACAGAGATGAAGAAATTCATATAGGTGATCATGTATCGCTACATAGTGCTCT	6120
Db	6061	GAAGTGTCACAGAGATGAAGAAATTCATATAGGTGATCATGTATCGCTACATAGTGCTCT	6120
OY	6121	CTGGGCTTTACCTTAGTGGGGAATGAAATTCGACCTGCAACTTGGAACTTACCTGAG	6180
Db	6121	CTGGGCTTTACCTTAGTGGGGAATGAAATTCGACCTGCAACTTGGAACTTACCTGAG	6180
OY	6181	TTTGAAGGACACCCCGGATATGTGAATGTGACATGTGCCAACAATATGACCTTGTGACGAC	6240
Db	6181	TTTGAAGGACACCCCGGATATGTGAATGTGACATGTGCCAACAATATGACCTTGTGACGAC	6240
OY	6241	TTCCAAGGCGTATCTTGAGCCAGAGCATCCCTGGAAAGCTATCCCAATTCCACAGCTGAC	6300
Db	6241	TTCCAAGGCGTATCTTGAGCCAGAGCATCCCTGGAAAGCTATCCCAATTCCACAGCTGAC	6300
OY	6301	TCTTGGCTGTGAGAGTGGAGCCGACCTATTAACATCTTCCCTCACAGTGGAGTACTTCTCTC	6360
Db	6301	TCTTGGCTGTGAGAGTGGAGCCGACCTATTAACATCTTCCCTCACAGTGGAGTACTTCTCTC	6360
OY	6361	AGCGAAGAACATATGATGAGTTTGAATTTTATATGTCTCATGAGGACAGAGTCTCTG	6420
Db	6361	AGCGAAGAACATATGATGAGTTTGAATTTTATATGTCTCATGAGGACAGAGTCTCTG	6420
OY	6421	CTGAAGGCCCTCAGTGGGAATTTACTCAGCTCCCTGATTTGTCACAGCTCAAGCAACTCT	6480
Db	6421	CTGAAGGCCCTCAGTGGGAATTTACTCAGCTCCCTGATTTGTCACAGCTCAAGCAACTCT	6480
OY	6481	GTGTACTGTGCTGTATCTGTATCAGCCTTACATGGAAGGGCTTCAAGATCGGTAT	6540
Db	6481	GTGTACTGTGCTGTATCTGTATCAGCCTTACATGGAAGGGCTTCAAGATCGGTAT	6540
OY	6541	TCAGGCCCTTACTGAGGCTGCGCCAGGGCTCACCTCCATGGCTTCACTTATGGCCAAACC	6600
Db	6541	TCAGGCCCTTACTGAGGCTGCGCCAGGGCTCACCTCCATGGCTTCACTTATGGCCAAACC	6600
OY	6601	AGCACCCAGCCCGGGGGCTTCATCCACTTTGGCTGTGCAAGCCGGCTACCGCTGTGGGA	6660
Db	6601	AGCACCCAGCCCGGGGGCTTCATCCACTTTGGCTGTGCAAGCCGGCTACCGCTGTGGGA	6660
OY	6661	CACAGCATGGCCATCTGTATCCCGGACCCCAAGGGCTATCAACCTGTGAGAGGAAGCCATC	6720
Db	6661	CACAGCATGGCCATCTGTATCCCGGACCCCAAGGGCTATCAACCTGTGAGAGGAAGCCATC	6720
OY	6721	CCTCTGTATAGCTCTTCTCTGTGGGCTTCTGTAGGCCCCCAAGAAATGGAATGTGT	6780

Db	6721	CCTCTGTGAAGTCTTTCTGTGGGCTTCTGTAGGCCCCAAGATGGATGGTGT	6780
QY	6781	GGCAAGAGTACACAGTGGGAACCAAGCCGTGTACAGTTGAGGCTACACCTC	6840
Db	6781	GGCAAGAGTACACAGTGGGAACCAAGCCATGTACAGTTGAGGCTACACCTC	6840
QY	6841	CAGCAGGCGGTGAGGGCATCTGCAGATGTCTGGACAAGGCCATATGGACACCGGAAT	6900
Db	6841	CAGCAGGCGGTGAGGGCATCTGCAGATGTCTGGACAAGGCCATATGGACACCGGAAT	6900
QY	6901	GTCCCAACAAGTGTGTC-----CTGTACTTGTCT	6933
Db	6901	GTCCCAACAAGTGTGTCCGTGAGTCTCGGGCAATGGAGCGGCTGTGTGCTTCT	6960
QY	6934	GATGTCAGTAGCATCAAGCTGGAGACATGGCCGATGAGGCTTATCTTTGACACAGTAT	6993
Db	6961	GATGTCAGTAGCATCAAGCTGGAGACATGGCCGATGAGGCTTATCTTTGACACAGTAT	7020
QY	6994	CAGTTTCCAGGCGCCAGCTGATGCTCATCTGTGGACCTTGGCACTACTACTATCTGCGCAAGG	7053
Db	7021	CAGTTTCCAGGCGCCAGCTGATGCTCATCTGTGGACCTTGGCACTACTACTATCTGCGCAAGG	7080
QY	7054	GTCAATCCGCTGTCAAGGCCAATGGCAATGGAGCTCGGAGACTTACGSCCACTTGCGCA	7113
Db	7081	GTCAATCCGCTGTCAAGGCCAATGGCAATGGAGCTCGGAGACTTACGSCCACTTGCGCA	7140
QY	7114	ATCATCTTCTGTGGAGAGCTCCCGATTCCGCCAATGGCAACGCGATCGGAACACTGTCT	7173
Db	7141	ATCATCTTCTGTGGAGAGCTCCCGATTCCGCCAATGGCAACGCGATCGGAACACTGTCT	7200
QY	7174	GTCTACGGGGCAACAGCCATCTTCTCCTGCATTCGCGGATACACACTGTGTGGGCTCCAGG	7233
Db	7201	GTCTACGGGGCAACAGCCATCTTCTCCTGCATTCGCGGATACACACTGTGTGGGCTCCAGG	7260
QY	7234	GTGCGTAGTGCATAGGCCAATGGGCTCTGGAGTGGCTCTGAAAGTCCGCTGCTT-----	7287
Db	7261	GTGCGTAGTGCATAGGCCAATGGGCTCTGGAGTGGCTCTGAAAGTCCGCTGCTTGGCACT	7320
QY	7288	-----	7287
Db	7321	CAGACCAAGCTCACCTCCATTTCTAATAGCTCCTTTCGATGACTCTTCCCACTCC	7380
QY	7288	-----GTGTGACACTGTGGGACTCTGTAGGCCATTGTCAAAGCACTAATAGGG	7338
Db	7381	CTCAACCAAGCTGAGCACTGTGGGACTCTGTAGGCCATTGTCAAAGCACTAATAGGG	7440
QY	7339	GAGAACTACAGCTACCGGGGCAAGTGTGTATCAATGACATGATGTGGCTTCGCGCTGATC	7398
Db	7441	GAGAACTACAGCTACCGGGGCAAGTGTGTATCAATGACATGATGTGGCTTCGCGCTGATC	7500
QY	7399	GGCATGTCTGTGCGCATCTGCACAGCAGATCATCACTGTGCGGCAAGACCCCTTTCTGT	7458
Db	7501	GGCATGTCTGTGCGCATCTGCACAGCAGATCATCACTGTGCGGCAAGACCCCTTTCTGT	7560
QY	7459	GTGC-----	7462
Db	7561	GTGCTATTTAAGCAGCAGTGTGCTGCTGCTGCTGTGTGTGTGTGTATGTATGATGAT	7620
QY	7463	-----CAATTACCTGTGGACACCACAGGCAACCTGTCAACCGGCTC	7503
Db	7621	GAAATGATGTGATGTGTGCAATTAACCTGTGGACACCACAGGCAACCTGTCAACCGGCTC	7680
QY	7504	ACTCAGGGTAAACAGTTTAACTTCAACGATGTGTCTCAAGTTTGTTTGCAACCTCGGCTAT	7563
Db	7681	ACTCAGGGTAAACAGTTTAACTTCAACGATGTGTCTCAAGTTTGTTTGCAACCTCGGCTAT	7740
QY	7564	ATGCTCTAAGGGGGCTGTAGGTCTCCAAATGCTTGCCACGCGGGCAATGAGTGAATGTCTG	7623
Db	7741	ATGCTCTAAGGGGGCTGTAGGTCTCCAAATGCTTGCCACGCGGGCAATGAGTGAATGTCTG	7800
QY	7624	CCGACCTGCAATCATCACTGTACGATCTGTGACACCAAGAAAATAGTGTTCGTGAC	7683

Db 7801 CCCACCTGCAGAAATCATCTACAGATCTGTGACACCAAGAAAAATGTTCTGAC 7860
 QY 7684 GTCCACGCGAGGGCCCGCAGAGTTCACTTGGGACCACTGCTTACCGGTGCAC 7743
 Db 7861 GTCCACGCGAGGGCCCGCAGAGTTCACTTGGGACCACTGCTTACCGGTGCAC 7920
 QY 7744 CACGGCTTCACTCTGCGGACCCAGTGTGACGTCGACGAGAGATGACATGGAC 7803
 Db 7921 CACGGCTTCACTCTGCGGACCCAGTGTGACGTCGACGAGAGATGACATGGAC 7980
 QY 7804 CGTCCCGCGCCCAAGTGTCTCT 7825
 Db 7981 CGTCCCGCGCCCAAGTGTCTCT 8002
 RESULT 11
 AAL49944
 ID AAL49944 standard; cDNA; 6004 BP.
 AC AAL49944;
 XX
 DT 10-DEC-2002 (first entry)
 XX
 DE Human molecule for disease detection and treatment coding sequence #18.
 XX
 KW Human; molecule for disease detection and treatment; MDDT; gene therapy;
 KW cytostatic; antiarteriosclerotic; hepatotropic; anti-HIV; anti-allergic;
 KW antiinflammatory; antiasthmatic; cerebroprotective; nootropic;
 KW neuroprotective; antiparkinsonian; cardiant; antianginal; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200270709-A2.
 XX
 PD 12-SEP-2002.
 XX
 PF 08-FEB-2002; 2002WO-US003709.
 XX
 PR 09-FEB-2001; 2001US-0268117P.
 PR 15-FEB-2001; 2001US-0269618P.
 PR 23-FEB-2001; 2001US-0271118P.
 PR 07-MAR-2001; 2001US-0274486P.
 PR 09-MAR-2001; 2001US-0274436P.
 PR 28-NOV-2001; 2001US-0334229P.
 PR 01-FEB-2002; 2002US-0353284P.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 PI Lal PG, Baughn MR, Yao MG, Walla NK, Elliot VS, Xu Y;
 PI Honchell CD, Yue H, Ding L, Gietzen KJ, Ison CH, Lu DM;
 PI Hafalia AJA, Ghadi AR, Thangaveilu K, Sanjanwala MM, Tang YT,
 PI Ramkumar J, Griffin JA, Swarnaker A, Azimzai Y, Sapperstein SK;
 PI Burford N, Lee EA, Lu Y, Tran UK, Marguis JP;
 XX
 DR MPI; 2002-713453/77.
 XX
 P-Psdb; AAO19415.
 XX
 PT New human molecules for disease detection and treatment (MDDT), useful
 PT for diagnosing, treating and preventing diseases or conditions associated
 PT with the aberrant MDDT expression, e.g. cancer, AIDS, asthma, diabetes,
 PT hepatitis.
 XX
 PS Claim 11; Page 174-176; 177pp; English.
 XX
 CC The present invention relates to human proteins and coding sequences of
 CC molecules for disease detection and treatment MDDT. The sequences can be
 CC used in the treatment of diseases associated with the decreased
 CC expression or overexpression of MDDT, such as cell proliferative (cancer,
 CC atherosclerosis, hepatitis), autoimmune/inflammatory (e.g. AIDS,
 CC allergies, Addison's disease, asthma), developmental (dwarfism, renal
 CC tubular acidosis), neurological (e.g. stroke, Parkinson's disease,
 CC epilepsy) and cardiovascular (congestive heart failure, myocardial
 CC infarction, angina pectoris) disorders. The present sequence is a coding

CC sequence of the invention
 XX
 SQ Sequence 6004 BP; 1272 A; 1795 C; 1615 G; 1322 T; 0 U; 0 Other;
 Query Match 42.0%; Score 4260.4; DB 6; Length 6004;
 Best Local Similarity 86.5%; Pred. No. 0;
 Matches 5175; Conservative 0; Mismatches 26; Indels 779; Gaps 12;
 QY 2571 TGGGAATTCATGACAGGACCTCAGGATCTTGTCTGTCTCCCACTTCTGTGAAC 2630
 Db 71 TTGGAATTCATGACAGGACCTCAGGATCTTGTCTGTCTCCCACTTCTGTGAAC 125
 QY 2631 CATATCAATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2688
 Db 126 CATATCAATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 184
 QY 2689 CTGAAGCCAGGACATTCGAACTCTGCGAGAGAGATGTCCTCAAGGTTTATGATGCAAC 2748
 Db 185 CTGAAGCCAGGACATTCGAACTCTGCGAGAGAGATGTCCTCAAGGTTTATGATGCAAC 244
 QY 2749 AACACTCCGCGCGCTTGTCTGCGAGGTTTATGATGATGATGATGATGATGATGATGAT 2808
 Db 245 AACACTCCGCGCGCTTGTCTGCGAGGTTTATGATGATGATGATGATGATGATGATGAT 304
 QY 2809 AACAGACATTCAGAGCTGCGGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2868
 Db 305 AACAGACATTCAGAGCTGCGGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 364
 QY 2869 GGGTTGAACCTGACCTTTTCAAGCTTGAATCATCATGATGATGATGATGATGATGATGATGAT 2928
 Db 365 GGGTTGAACCTGACCTTTTCAAGCTTGAATCATCATGATGATGATGATGATGATGATGATGAT 424
 QY 2929 AAGTTGGCTACAGGTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2988
 Db 425 AAGTTGGCTACAGGTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 484
 QY 2989 TGTGACCTGGAATPACAGCTGCGGGGTATGAGAGCTGCTGTGTGATGAGAGCCG 3048
 Db 485 TGTGACCTGGAATPACAGCTGCGGGGTATGAGAGCTGCTGTGTGATGAGAGCCG 544
 QY 3049 CCGACCTGGAGACCGGCTCTGCGCACTGTGTGCGCGAGTGTGAGAGGACAGTGAAGGA 3108
 Db 545 CCGACCTGGAGACCGGCTCTGCGCACTGTGTGCGCGAGTGTGAGAGGACAGTGAAGGA 604
 QY 3109 GAGGTGTGCGGGGAGGTGCTGTACCGGGGTATTCAGCTTCTGTGAACAATCTCAAC 3168
 Db 605 GAGGTGTGCGGGGAGGTGCTGTACCGGGGTATTCAGCTTCTGTGAACAATCTCAAC 664
 QY 3169 TGCATCTGGAACATGGAAG 3228
 Db 665 TGCATCTGGAACATGGAAG 724
 QY 3229 GACACAG 3288
 Db 725 GACACAG 784
 QY 3289 CTGCTGAAG 3348
 Db 785 CTGCTGAAG 844
 QY 3349 GTGCTGCTGAGTTCAGACCTGATCTTTCACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3408
 Db 845 GTGCTGCTGAGTTCAGACCTGATCTTTCACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 904
 QY 3409 TAGTGTTCACAGCAAGCTGTCATATGACCTTGGATCCCGCAGAAATGGAGTGGAGT 3468
 Db 905 TAGTGTTCACAGCAAGCTGTCATATGACCTTGGATCCCGCAGAAATGGAGTGGAGT 964
 QY 3469 GGTGACAGTTGGAGAGCGGCGCATTCACAGTGTTCAGTGTGACCTTGGAGTGGAGT 3528
 Db 965 GGTGACAGTTGGAGAGCGGCGCATTCACAGTGTTCAGTGTGACCTTGGAGTGGAGT 1024
 QY 3529 CAGGGAAGTGCAGAGATGCTGTGTGAAAGATCGAAGACAGGTTCTTCTGGAGAGCCACG 3588

Db	1025	CAGGGAAATGAGAAATCAAGCTGTGTGAAGATCGAAGACAGATTTCTTGGACGCCAGC	1084
Oy	3589	CCGGCAATCATCATGCTCTCCTTCGGGGGAGACCTGACAGACCAATCTGAGTCAATCCTC	3648
Db	1085	CCGGCAATCATCATGCTCTCCTTCGGGGGAGACCTGACAGACCAATCTGAGTCAATCCTC	1144
Oy	3649	TCACCAAAATTATCCCGAAGCCCTTACCCCGCAGGCAAGAGTGTACTGTAAAGTACCCGT	3708
Db	1145	TCACCAAAATTATCCCGAAGCCCTTACCCCGCAGGCAAGAGTGTACTGTAAAGTACCCGT	1204
Oy	3709	TCACCAAGCTATAGTCAATGAGCCCTGGTATTTTAAATCATCTTAACTGTAGACCTGGCTATGAC	3768
Db	1205	TCACCAAGCTATAGTCAATGAGCCCTGGTATTTTAAATCATCTTAACTGTAGACCTGGCTATGAC	1264
Oy	3769	TTCTCTCATATCTACGACGAGACGGGACTCTCTCAGCCCTCTCATAGAAAGCTTCTATGGC	3828
Db	1265	TTCTCTCATATCTACGACGAGACGGGACTCTCTCAGCCCTCTCATAGAAAGCTTCTATGGC	1324
Oy	3829	TCCCAAGCTCCCCAGGCGGATGTTAAAGACAGCAACACCTCTTCTGTGGCTTCCGACGC	3888
Db	1325	TCCCAAGCTCCCCAGGCGGATGTTAAAGACAGCAACACCTCTTCTGTGGCTTCCGACGC	1384
Oy	3889	GATGATCTGTGAGCAATGCTGGCTCGTCAATTCATCTTACAGAAAACCCCGGGAGTCA	3948
Db	1385	GATGATCTGTGAGCAATGCTGGCTCGTCAATTCATCTTACAGAAAACCCCGGGAGTCA	1444
Oy	3949	TGTTTGTATCTGTGTTCCATCAAGACGGCACACGGGTGGGGTCCGACTTAAGCTGGGC	4008
Db	1445	TGTTTGTATCTGTGTTCCATCAAGACGGCACACGGGTGGGGTCCGACTTAAGCTGGGC	1504
Oy	4009	TCCTCCGACCTCACTACTATGCGCACGGGGGGCTTACGAAAGTTGAGGGACCTCGACCTGAGC	4068
Db	1505	TCCTCCGACCTCACTACTATGCGCACGGGGGGCTTACGAAAGTTGAGGGACCTCGACCTGAGC	1564
Oy	4069	TGCATCTCTGGGGCTGATGAGGAGGCCGCTGTGTGAACAATTCGCCGGCCAGTCTGCACAGCC	4128
Db	1565	TGCATCTCTGGGGGGCTGATGAGGAGGCCGCTGTGTGAACAATTCGCCGGCCAGTCTGCACAGCC	1624
Oy	4129	CCCTGTGGGGGACAGTATGTGGGTTCCGACGAGTGTGTTGTCCCCCACTAACCCCCAG	4188
Db	1625	CCCTGTGGGGGACAGTATGTGGGTTCCGACGAGTGTGTTGTCCCCCACTAACCCCCAG	1684
Oy	4189	AACTACACAGTGGACAGATCGCTGTATTTTGTACTGTGCGCCCAAGACATATGTGTG	4248
Db	1685	AACTACACAGTGGACAGATCTGCTGTATTTTGTACTGTGCGCCCAAGACATATGTGTG	1744
Oy	4249	TTTGGCCAGTTTCGCTCTTTTCAACGGGCCCTCAACGACGTGTGAGAGTTTACAGACGGC	4308
Db	1745	TTTGGCCAGTTTCGCTCTTTTCAACGGGCCCTCAACGACGTGTGAGAGTTTACAGACGGC	1804
Oy	4309	CACAGCCAGCACTCGGGCTCTGAGCTCCCTTCGGGCTCCCAAT	4354
Db	1805	CACAGCCAGCACTCGGGCTCTCTCAGCTCCCTTCGGGCTCCCAATCAGTATCCGGGC	1864
Oy	4355	-----	4354
Db	1865	TCGGCCATGTGGGAGTGTGTGTGGCCGGGGGACATCAGTCCGGCTAAAGAAAGAGGC	1924
Oy	4355	-----	4354
Db	1925	TCTAGAACACCCCATGTGCGCGAGGTGGAACCTTACGGCTCTGCGTGTGCTGTCT	1984
Oy	4355	-----	4354
Db	2045	AGCTGCCCTCAACCCAGACTGTGTCTACAACGCCCCCTTGTGTGTAGCTTCTCTGTGTG	2104
Oy	4355	-----	4354

[illegible]

OY	5332	TACGACCTTCAATAGAAATCCCGAATAGGCCCTCTATGACACACCCGATGATGGGAATTC	5331
Db	3245	CACGACTACATAGAAATCCGGAATAGGCCCTCTATGACACACCCGATGATGGGAATTC	3304
OY	5392	AGTGGAAACGAGCTTCCAAAGCTCCCTCTCTCAAGTCCCAAGACCAACCGTATATTC	5451
Db	3305	AGTGGAAACGAGCTTCCAAAGCTCCCTCTCTCAAGTCCCAAGACCAACCGTATATTC	3364
OY	5452	CACAGCGACCACTCCCAAGATCGGCAGAGATTCAAGCTGGAGTACG-----	5499
Db	3365	CACAGCGACCACTCCCAAGATCGGCAGAGATTCAAGCTGGAGTACGAGATTGACTTAC	3424
OY	5500	-----	5499
Db	3425	TCGCCACAGATTTCTTCTCTAGAGTTTGTATCTCTGGAGTTGGAAAGAACACAC	3484
OY	5500	-----GCGTAT	5505
Db	3485	TCAACTCTCCCGTCGCGCTTCTCTATGTCTGGATCTTGATCTGTTGTTGGAAGCTAT	3544
OY	5506	GAACTTCAAGAGTCCCGACAGCCGAGGCCCTTTCGCAATGGCAATTGGAGGGAGCTGCG	5565
Db	3545	GAACTTCAAGAGTCCCGACAGCCGAGGCCCTTTCGCAATGGCAATTGGAGGGAGCTGCG	3604
OY	5566	TACAACTGGGACATCAGTACCTTCAGTGCCTCCGGGGTATCAATTATCAGGCAC	5625
Db	3605	TACAACTGGGACATCAGTACCTTCAGTGCCTCCGGGGTATCAATTATCAGGCAC	3664
OY	5626	CCTGTCTCAGCTGTCAACATGGGACCAACCGGAATGGGACCAACCCCTGCGCAAGTGT	5685
Db	3665	CCTGTCTCAGCTGTCAACATGGGACCAACCGGAATGGGACCAACCCCTGCGCAAGTGT	3724
OY	5686	GAAGTCCCTTGTGGGGGGAACATCACTTCTTCCAAACGGCACTGGTACTCCCGGGGTTTC	5745
Db	3725	GAAGTCCCTTGTGGGGGGAACATCACTTCTTCCAAACGGCACTGGTACTCCCGGGGTTTC	3784
OY	5746	CCTAGCCCGTACTCCAGGCTCCCAAGACTGTGTCTGGCTGATCACCGTGCC--ATTGC	5802
Db	3785	CCTAGCCCGTACTCCAGGCTCCCAAGACTGTGTCTGGCTGATCACCGTGCCCAATTGGCC	3844
OY	5803	CATGGCCGTCCGCTCAACCTGACCTGTGGAGACAGAGCCCTTGGAGATTTGATCAC	5862
Db	3845	ATGGCCGTCCGCTCAACCTGACCTGTGGAGACAGAGCCCTTGGAGATTTGATCAC	3904
OY	5863	ATCTGGATGGGACCAAGCAAAACAGACACAGGCTCGCGTCTTACCCGGAGCATGGC	5922
Db	3905	ATCTGGATGGGACCAAGCAAAACAGACACAGGCTCGCGTCTTACCCGGAGCATGGC	3964
OY	5923	AAGAAAACAGTGCAGAGTTTATCCACAGGTCCTGCTCAAGTTTCAACCTGATGACGCC	5982
Db	3965	AAGAAAACAGTGCAGAGTTTATCCACAGGTCCTGCTCAAGTTTCAACCTGATGACGCC	4024
OY	5983	ACAGGGGGGATCTTCGACATAGCTTTCGCGTTATCCACTACCAATAGCCCTCTCCC	6042
Db	4025	ACAGGGGGGATCTTCGACATAGCTTTCGCGTTATCCACTACCAATAGCCCTCTCCC	4084
OY	6043	ACCATCTCTCCCAAGCCGGAAGTCGTCAAGAGATGAAGATTCATATATAGTGAATC	6102
Db	4085	ACCATCTCTCCCAAGCCGGAAGTCGTCAAGAGATGAAGATTCATATATAGTGAATC	4144
OY	6103	GTAAGCTTCAATAGCTCTCCCTGGCTTTCCTTAATGGGGAAATGAATTTCTGACTGCATA	6162
Db	4145	GTAAGCTTCAATAGCTCTCCCTGGCTTTCCTTAATGGGGAAATGAATTTCTGACTGCATA	4204
OY	6163	CTTGGAACTTCTGACAGATTCACACAGGCTGATCTGGAACGAGACTTACTGGAAGCTAT	6222
Db	4205	CTTGGAACTTCTGACAGATTCACACAGGCTGATCTGGAACGAGACTTACTGGAAGCTAT	4264
OY	6223	AATGAGCTTCTGACAGATTCACACAGGCTGATCTGGAACGAGACTTACTGGAAGCTAT	6282
Db	4265	AATGAGCTTCTGACAGATTCACACAGGCTGATCTGGAACGAGACTTACTGGAAGCTAT	4324

[illegible]

Db 633 CACGGGACAGGGGTTCAACATCATATACACACATTTGGTTCAGAAAGCATGTTCATGACCC 692
 Qy 1359 TGGCGTTCCAGTAATAAGGAAACGGTTTGGGACACCTCCAGCTGGGAGCTCCATCTC 1418
 Db 693 TGGGATCCCTGTGAATGGAACGGGCTTTGAGACAGATTTCTGGGAAAGTTCTGTGTC 752
 Qy 1419 CTTCCTCTGTGATGAGGCTTCCCTTGGAGCTCAGGGCTCAGAGACCATCAGCTGCTCT 1478
 Db 753 CTTCACCTGTGATGATGCTTTGTGTAAGACTCAGGGTCTGAGTCTATCAGATGATCTT 812
 Qy 1479 GAAGAGGACAGCGGTGTCTGAAACAGCGCTGTCTGCGGTGAAAGCTCCCTGTGTG 1538
 Db 813 GCAAGATGAAAGTGGTCTGAGAGCTCTACTGCTCCGCTGGAGAGCTCTGTGTGTG 872
 Qy 1539 TCACCTGATTTGGCCCAAGGACCATCTCTCTCCGGGCTGGGCTTGTCTACAAAGA 1598
 Db 873 GCATCGACAGCTTCTAGTGGGGTCAATATTACTCCAGATGGCCAGGATATTACAAAGA 932
 Qy 1599 TGGCTTGAAGCTGCTGGGATGATGAGGCGCCAGAGGCTACCCCATCAAAATCAGCTT 1658
 Db 933 TTTCTTAAATTGGGAATGGGTCTTTAAGCCAAACAGACATTCATCAAAATTAACATT 992
 Qy 1659 CGACAGATTCAAAACCGAGGTCACTATGACACCTGGAAGTACGGGATGGGCGGACTTA 1718
 Db 993 TGAAGATTCCAGACAGAAAGTCAATTATGATCTTGAAAGTCCGGGATGGGCAACAG 1052
 Qy 1719 CTGAGGCGCTTGTATGGGGTTTACACGGGACCCAGGTTCCCAAGTTCTCTATCGAC 1778
 Db 1053 CTCATCCCACTGATTTGGGAGTACATGACCCAGGCTCCACAGTCTCTATCGACAC 1112
 Qy 1779 CAGCACTACCTCTACCTCTCTCTCTACCGAAGAGTCACTCGGACATCGGCTTCCA 1838
 Db 1113 AGGAACTACATTAATTAATCTGTTTACACTGACAGACCGGCTGAGTGTGCTTCT 1172
 Qy 1839 GCTCCGCTATGAGACTATTAACCTGAGTCAAGCACTGTGATTCAGGAATCCAGT 1898
 Db 1173 CATCACTATGAGAGTGTACTTGTATCTGATCTGCTGTGGAACCGGGCATTCCTGT 1232
 Qy 1899 AATGGAACAGCTCAGGGAATGACTTCTACGTGGGCGCTGTGATCTTCACTGTGTA 1958
 Db 1233 AATGTGATCGGACAGGAGTAACTTTGGTATCAATCTACAGTACCTTCACTGTGTA 1292
 Qy 1959 CTCGGGCTACACATTAAGTGAAGGGAGCCTCTGAGTGAAGCCCACTTCCAGTGAAG 2018
 Db 1293 CCTGGGTACACCTCAGATGATCAATCCCTCCTCCTGAGAAAGAACATCAGTGA 1352
 Qy 2019 CCGGGCCCTGCGCAGTTGTGAAGCTCTGTGTGGCTTCACTCAAGGCTCCAGTGGAC 2078
 Db 1353 CCAAGCTTGGCCAGCTGTGATGCCCTGTGTGAGGCTACATCCATGGAAGAGTGGAC 1412
 Qy 2079 CATCTGTGCGAGGGTCCCTGATCTTCAACCCCAACATGAACTGACCTGATTAAT 2138
 Db 1413 TGTCTTTTACAGGAATTTCCAGACTTTTATCCAACTCTGAACTGTACATGACAT 1472
 Qy 2139 CGAAACATCTCAGGAGGAGTGTCTTCACTTTCCAACTTCCAACTTCCAACTGGAAGT 2198
 Db 1473 TGAAGTCTCTCAGGAGGAGTGAAGATGAATTTCCACACTTTCACTTAAAGTTC 1532
 Qy 2199 CCACTGACTACCTCTCTCATCTAGAAACGAGAGCTTCAACAGCCCTCTGAGAGCTAAC 2258
 Db 1533 CCAAGACTATTTGCTATCAAGAGATGGAGTTTCTCAGACCCGATGAGGCTCAC 1592
 Qy 2259 TGGATCTCGGCTGCGAGCTCCATCAGCGCTGGGCTCTATGCACTTCTGCGCAAGT 2318
 Db 1593 TGGGTGGTCTGCTGCTCAACACATTAAGGCTGGCTGTGTTGAAACTTCACTGCGCACT 1652
 Qy 2319 CCGCTTCTATCTGATTTCTCCATGTCATATGAAGATTAACATCACTTCCAGAGTA 2378
 Db 1653 CAGATTCATCTGACTTCTCACTCTCATGAAAGGCTTCAAACTTAAGTTGCAAGATA 1712
 Qy 2379 CCACTTGAAGCCCTGTGAGAGCCGAGGCTCCAGCTTACAGCATCCGGAAGGCTTGA 2438
 Db 1713 TGAACTAGAACCTGTGATGACCTGTGAGTCCCTGCTTACAGTCCGAGAAATTTGGTTCCA 1772

Qy 2439 GTTGGCGTGGGCGACACCTTGAACCTTCTCTGCTTCCCGGGTACCGTCTGAGAGGAC 2498
 Db 1773 GTTCGATGTGGGTGACACCTTGTCTTCACTGCTTCCAGGATACCGCTTGAAGGTGC 1832
 Qy 2499 CGCCCGCATCAGTGTCTGGGGGAGACAGGCGCTGTGAGCTGCTCTGCCAAGTG 2558
 Db 1833 AACCAAGCTTACCTCTGTGGTGGGGAGCCGAGTGTGAGTGAACCTCTGCCAAGTG 1892
 Qy 2559 TGTGCTGATGTGGGAATTCAGTCAAGGACCTGAGGTACTTGTGTGCCCACTT 2618
 Db 1893 TGTGCTGATGTGAGCAAGGCTCAAGGAATGAAGGAATTAATCTTCCAAATTT 1952
 Qy 2619 TCCCTGAACTCAATTAACATCAATGAATGATCTACTCTCACTCAGACCCAGGAGA 2678
 Db 1953 CCCATTCAAATTTGATTAATTAACATGAGTGTATCTTAATAATGAAGAACGAGGAGA 2012
 Qy 2679 GGGAAATTCAGTGAAGCCAGGAGCATTTGCACTCTCGAAGGAGATGTCCTCAAGTTTA 2738
 Db 2013 GGGGATCCATCTCAGAGCCGGAACCTTCCACTTTCGAAAGGACACTCTAAAGTTTA 2072
 Qy 2739 TGAATGCAACAACTCCGCGCTTGTGTGGAGTTTACCATTTGATGATGATGG 2798
 Db 2073 TGAATGAAAGACAGCTCTCTGAGGTCACTGGAGTCTTCAAGAGTGAACATGATGG 2132
 Qy 2799 GGTGACTTTGAACAGACATCCAGCAGTGTGTGGCTGATTTCACTCATGATGCTGA 2858
 Db 2133 GCTGTGCTAAACAGACCTTCCAAACACTGAGGCTGAGGTTCACTTAAGGGTCA 2192
 Qy 2859 CACACAGAGGCTTTGAACCTGACCTTTTCAAGTTTGAACATCAATCAATGAAGACC 2918
 Db 2193 TACCGCCCAAGCTTCCAGCTCACTCACTACAGAGTTTGAATGAATGAAGATCC 2252
 Qy 2919 AGGAACCCCAAGTTTGTGTAAGGTTATGATGAAGTCAATTTGACGAGAGCTCCGT 2978
 Db 2253 AGGCAATCCCTTAATGTGCTTACAGATCCGAAATGATGTCACTTCAAGACACTGTGT 2312
 Qy 2979 GTTCCTTCACTGTGACCTCGAATPACAGCCTGGGGGTATGAGAGCTGTGTGTGAG 3038
 Db 2313 TCTTACAGCTGACACCGAGCTGACATGATGACAGACAGTACCTTACCTGCTGAG 2372
 Qy 3039 TGAAGACCGCGGACCTGTGAGACCGGCTCTGCGCACTGTGTGCGAGTGTGAGAGGAC 3098
 Db 2373 TGGGACCGAAGGTGTGGGACAAACATATGCTTCTGTGTGGGAAATGTGTGTCT 2432
 Qy 3099 AGTGAAGAGAGGTGTGCGGCGAGTGTGACACCGGGTATCCAGCTTCCATGAACA 3158
 Db 2433 CGTCCATGAGCCACATCAGAGACGATACTCTCTGCTGCTACCTGCCCATATGACAA 2492
 Qy 3159 CAATCTCACTGATCTGAGACATGAGAACAGAGCGCGGCTGACCATTTGGGCTACAT 3218
 Db 2493 CAACCTTCAATGACTTGAACATGAGGCTGATCTTGGCAAGACCAATGAGCTTCAAT 2552
 Qy 3219 CCTGTGTTTGAACAGAGAGGTTTCAACAGCTGTGCGCATCTGGGATGGGCTGTGGA 3278
 Db 2553 CATGTGTTTGAACAGAGAGGTTTCAACAGCTGTGCGCATCTGGGATGGGCTGTGGA 2612
 Qy 3279 GAGCGGGGTTTGTCTGAAGAGCTGAGTGTGAGGCGCGCTGCGCAAGACCTGATGAC 3338
 Db 2613 CAGCAACATCTGTGTAAGAGAGTGTGAGGCGGCTTCCCTGAGAGACATCCACAGCAC 2672
 Qy 3339 CTTCACCTGGTGTCTGTGAGCTGACATGACATCTTCCACAGAACAGAGGCTTTCG 3398
 Db 2673 CTTCACCTGGTGTCTGTGAGCTGACATGACATCTTCCACAGAACAGAGGCTTTCG 2732
 Qy 3399 CATTCATTTTCAAGTGTCCACAGACAGTCTGCAATGACCTTGGGATCCGCAAGATG 3458
 Db 2733 CATCAGTTCTCTACTTCCATTTGATGATCCAGCTGCAATGACCTTGGGATGCTCAGATG 2792
 Qy 3459 GAGTGGAGTGTGACAGTTTGAAGCCGAGCATCTCAAGTGTTCAGTGTGACCTTGG 3518
 Db 2793 AACCCGTATGTGACAGCGGGGAACCTGGAACACATCACTTCCAGTGTGACCTTGG 2852

QY 3519 CTACGGCTGACAGGAAGTGCAGAGATCAGTGTGTGAAGATCGAAGACAGGCTTCTTG 3578
DB 2853 ATACGAGCTCCAGGGGACAGCCAGATCACTTGTGTGAGCTTAAACAACGCTTCTTG 2912
QY 3579 GCAGCCGACCGGCAACATGCATCGCTCCGCGGGAGACCTGACAGAACATCTTG 3638
DB 2913 GCAACGAGACCTCCCTCATGTAGCTGCTGTGTGGGAACTGACAGGCGCTGCTG 2972
QY 3639 AGTCATCCCTCAACAAATTTACCCAGACCTACCCGCGAGGACGAGATGAGCTGGA 3698
DB 2973 AGTGAATTTATATCCCAACTACCCACAGCATACCTCTGGGAGAGATGTGACTGAG 3032
QY 3699 AGTACCGCTCTCAACGAGCTAGCTCATCGCCCTGTATTAAATCTTTAACTGAGCC 3758
DB 3033 AATTAAGTGAACCCGACTTTGTCTATGTCTTAATTTCAAAAGTTTAAAGTAGAGCC 3092
QY 3759 TGGCTATGACTTCTTCATATCTACGACGAGAGGAGCTTCTGAGCCCTCATAGGA 3818
DB 3093 AAGTACGACTTCTGCAATCTATGTAGAGGAGAGCTCAACAGCCACTGATCGAAG 3152
QY 3819 CTTCATGAGCTCCAGCTCCAGGCGCATTTGAAAGCAGACAGCTCTTCTGCG 3878
DB 3153 CTTCAGAGGTTCTCAAGCCCAAGAGATGAGAGCATGTATACAGCTTCTCTGCG 3212
QY 3879 CTTCGCGACGATGATCTGTAGCAATGCTGCTTCTCATTTGAATATACAGAAACCC 3938
DB 3213 ATTCAGAGATGATGCTCTGTTGGCTGTCCGGGTTTGCATTGAATTTAAAGAGAAC 3272
QY 3939 GCGGAGTATGTTTGTATCTGTGTTCCATCAAGAACGAGCAACGAGGTGAGTCCGACT 3998
DB 3273 AGGGGAGGTTCTTGTGACCTGAGGAACTAATGAAAGGAGATTTGAAACGAGACT 3332
QY 3999 GAAGTGGGCTCTCCGCTACCTACTAGCCAGGAGGCTAGAGATGAGGAGCCG 4058
DB 3333 TAAAGTGGCTCTCAAGTTACTATCAATGTGACTGTGTAAAGATTTGTGATCTTC 3392
QY 4059 GACCTGAGCTGATCTGAGGAGCTGATGAGAGCCGCTGTGAAATATCCCGGCACT 4118
DB 3393 ATTCATGAGTGTGAGACAGGGAGCTGATGGAAGCCGCTGGAACCGGCGACTGCG 3452
QY 4119 CTGCACAGCCCTGTGTGGGAGACATGTGGGTTGAGACGAGTGTCTTGTCCCA 4178
DB 3453 CTGCCAAGACCTGTGAGAGGCAATACATGAGCTGAGAGGGGTATGTTGTACAA 3512
QY 4179 CTACCCCGAGACTACACAGGTGAGACAGATCTGTTGATTTTGTATCTGAGCCAA 4238
DB 3513 CTACCTCTATATCTACAGGCTGGGAGATATGACTATTTCTATCAACGATGCCA 3572
QY 4239 CTATGTGTGTTTGGCAAGTTGCTTTTCAACGAGCCCTCAACGAGTGTGAGAT 4298
DB 3573 ATTTGTGTGTTTGGACAGTTTGGCTATTTCCAGACTGGGCTGAACGACTTGGCA 3632
QY 4299 TCACGACGCGCACAGCCAGACTCGCGGCTCTGAGCTCTCTGCGGCTCCCATACAG 4358
DB 3633 GTTTATGAGAACCAATCTCAGAGCGAGCTTCTGAGTTCTCTGTGTCCATTCAG 3692
QY 4359 AGAATCACTGACCTTGGCACTCTCAATCAAGTTCTCATTTAGTTCAAGGCAAGGCT 4418
DB 3693 TGAACACTCCCGCTGGCTACATTCATCAATGATTTGCTTGGCTTCAAGGCAAGGCG 3752
QY 4419 GCGACAGCAGAGGCTTCACTTTGTCTACCAAGCGGTTCTGCAACGAGCCAGCA 4478
DB 3753 AGCTTCTGACAGGGGTTTCACTTGTCTACCAACCGTCCCAACGAGTGAACGCA 3812
QY 4479 GTGCAAGCTCTGTGCGGGAACCCGCTATGCAAGAGGCTGGGAGTGTCTGAGTGG 4538
DB 3813 GTGCAAGCTCTGTGCGGGAACCCGCTATGCAAGAGGATGTGTTCTGAGTTCTGCA 3872
QY 4539 GGCATCTGCTGCTTGAATGCAATCGGCTATGCTCCCTGCAAGGAGTGGCAGAGATGA 4598
DB 3873 CTTCATCTGCTGCTTGAATGCAATCGGCTATGCTCCCTGCAAGGCTCAACGAGTCC 3932
QY 4599 GTGCTCTGCTGCTGAGGAGCTTGGCCCAATGAAATGTCTCAAGCCCAAGTGTGTGT 4658

DB 3933 TTGTAGCTGTGTGCCAAACGCTTTTGGCCAGTGGAAATACACATCCCAAGCTGTGTAGT 3992
QY 4659 GCGGTGTGAGGCAACTACAGAGCGAGGCAATCTGTTCCCTGCTTCCAGA 4718
DB 3993 TCATGAGTGTGCAATTTCACTCAGAGAGAGGCAATCTTATCTCCAGGCTACCTGA 4052
QY 4719 GCGGTACTCAACAGGCTCAACTGTGTGTGGAAGATGTGTGTCCCGAAGGCGGTGAT 4778
DB 4053 GCGCTTATGGAACAACCTGAAGTGTATGGAAGTCAATGATGTGAGGAGCTCAGGAT 4112
QY 4779 CCAGATCCAGATGTGCACTTTGTGACAGAGCAGAACTGGGACTCGTGAAGTATTTGA 4838
DB 4113 COAGATCAAGTATGATTTAGCTTTGCAACGAGACAGAACTGGGACTCCGAGATCATGA 4172
QY 4839 TGTGCAATTAACATGTATCACTGTGGGAGTTTCTCAGAAACACCTGCTGCTCT 4898
DB 4173 CGAGGAGACATGACGCGCCCAAGCTGGGCAAGCTTCAAGTATCACAGTGCAGCACT 4232
QY 4899 TGTGAACGACCTTCCAAACGAGCTTACCTTATTTCTACTCAGATATCAGGTATGCG 4958
DB 4233 GCTGATATGCACTTCAACAGCTCTGTGCACTTCCAGTGGACATCACTGTGCGCG 4292
QY 4959 AGCTGGCTTCCACTTGAAGTCAAAACGAGTGGGCTGAGCACTTGTCCGAACTGTGT 5018
DB 4293 TCGCGGCTTTCACTGGAATCAAAAAGGTGGTGTGCTGGCTGGGCGAGAACCTGCTCT 4352
QY 5019 GCCCATGACGGGATGAAGATGCGAGAGCTTACTTGTGATATGATGTGTCTTTCA 5078
DB 4353 CCCAGCAACGGCATCAAGATGAGAGACCGCTATATGTGTGAACATGTGCTCTTCA 4412
QY 5079 GTGTGAGCGGGATATGCGCTCCAGGGGCAAGGCCCACTCCCTGCAATGCCGGAACGT 5138
DB 4413 GTGGAAGCTGTGATACCTTTGACAGGCGCTCTCAACATTTCTGTATGCGGAACTGT 4472
QY 5139 GCGGAGATGAATACCTCTCTCACTGTATTTGCAACAGTGTGGGGAACAGTGAAGA 5198
DB 4473 ACGTGTGGAATATCTCTTCCCTGTGTGATGCACTGTGTGGGACACTGACAG 4532
QY 5199 GATGAGAGGGGTATCTGAGAGCCCGGCTTCCAGGCAATCAACCACTGAGACTG 5258
DB 4533 CATGATGAGATGATCTGAGACCCAGGCTTCCAGGCTCAATACCCCAACCTGAGCTG 4592
QY 5259 CTCTGGAATAATACACATGCGCGGTGGGCTTGAAGTCACTCCAGTTCTGAACTTCTC 5318
DB 4593 CACTGGAAGTATCTCTGCGCAATGAGTATGATGATGATCAATTTCTGAATTTCTC 4652
QY 5319 CACGAGCCCAACGAGACTACATAGAAATCGGAATGCGCTATGAGACAGCGCAT 5378
DB 4653 AACTGAAGCCAAACATGACTCTGAGATCAAGATGAGGCTTACCACTAGTCCAT 4712
QY 5379 GATGGAAGATTTCAAGTGAAGAGGCTTCCAGAGTCTCTCTTCCAGTCTCCAGAGAC 5438
DB 4713 GATGGAACAGTTCAAGTGGGCTTCACTGCTGCTCACTGTGAGCAACACATGGAAC 4772
QY 5439 CACGATATTTTCAACAGGCACTCTCCAGAAATCGGCAAGATTTCAAGTGAATCA 5498
DB 4773 CCTATCTGCTTCTATATGATCACTCAGAACCCGAGATTTTAACTCACTTACCA 4832
QY 5499 GGCCTATGAACCTTGAAGAGTCCCAACCCAGAGCCCTTGGCAATGAGATGTGAGGG 5558
DB 4833 AGCTTATGAGTATCAGAAATGCGCGGACCCAGCCGATTCAGAAATGGGTTCAATGACA 4892
QY 5559 AGCTGTGCTAACAAGTGGAGCAATATGATGACTTGTGAGTGTCTCCGGGATTCATTTGAC 5618
DB 4893 CTTCGATTTACAGCTGTGGCCAGTGTGATCTATTTGAGTGTCTACCCGGGCTACATCTTGTCT 4952
QY 5619 TGGCAGCCCTGTCTCTCACTGTGCAACATGGAACCAACGGAATCGGAGCAACCCCTGGC 5678
DB 4953 AGGCACTCTGTGTCTCACTGTGCAAGTGTGCACTGAGAGAACTGGAATCACTTCTTCC 5012
QY 5679 CAAGTGAAGTCTCTTGTGGGAGGAACTCACTTCTTCAACGGACTGTGTACTGCC 5738

Db 5013 ACGGTGTGACGCTCCTGTGGTATATGATCATCAGAAATGGACCATTTATTTCCCC 5072
QY 5739 GGGGTTCCTTAGCCCTTACTCCAGCTCCAGAACTGTGTCTGCTGATACCGTGGCCAT 5798
Db 5073 TGGGTTCCTAGAGATATCCTCAATTTCTGAAGGACTGCTGTGTGTGATCATGTCTCC 5132
QY 5799 TGGGCTAGGCTCCGCTCAACTCAGCCCTGTCAGAGACAGACCCCTGTGAGATTTCAAT 5858
Db 5133 AGGACATGAGTGTATCATCACTTCACTTGTGCAAGCTGAGGCTGTAAATGATCAAT 5192
QY 5859 CACCATCTGGAGTGGCCACAGCAACAGCACGCGCTGGGTCTTCAACCCGAGCAT 5918
Db 5193 CGCTGTGGAGTGTCTGACAGAACTGCTCAGCTCGGGGTCTTCACTGGAACAC 5252
QY 5919 GGGCAAGAAAACGTGACAGTTTCACTCAACCGGTCTGTCAAGTTTCAACCGTATGC 5978
Db 5253 TGGCTGTGAGACAGATACAGCTCCACCAACGAGGCTTGTCTCAATTTCCACGCGCATTT 5312
QY 5979 AGCCACAGGGGGGATCTTCCGCTAGCTTTCTCGCTTATCCACTCACCMAATGGCCCTGC 6038
Db 5313 CTCGAATGGAGCTTCTTGTGTCTCAATTTTCAATGATTTCACTGAAGAGTGGCCGCC 5372
QY 6039 TCCACCATCTTCCCAACGCGCAAGTGTCTCACAGAAATGAAGAAATTCATATAGTGA 6098
Db 5373 TCTTCAGATAGTCCGACAGGCTGACCTGCTTACAGAAAGATGAAGACTTTGAATAGGGGA 5432
QY 6099 CATCTGACGTACAGATGCTCTCCCTGTCTTACCTTATAGTGGGAATGAATTTGACCTG 6158
Db 5433 CTTCGTAAGTACCAAGTGCATCCAGGATACAGCTGTGGGAAGTGAACCCCTGACATG 5492
QY 6159 CAAACTTGAACCTTACCTGATTTGAAGAACCAACCCGATATGTAAGTGCAGTGC 6218
Db 5493 CAACTCAGCTCAGCTATTTGTTCAAGGCTTCCACTTCTGTAAGACACATATGCC 5552
QY 6219 AACAAATGAGCTTCTGACAGACTCAAGCGGTATCTGAGCCAGAGCTACCTGGAAG 6278
Db 5553 AGCCATGAGTGCAGAGTCTTCTGGGTGATTTCTCAGTCTGGGTACCCAGGCA 5612
QY 6279 CTATCCCACTGACAGCTGCTGTGTGTGAGAGTGGAGCCGATATACATCTC 6338
Db 5613 CTATTTTAACTCCCAACATGTGCTTGAATTTAAAGTGAAGCCAACTTTAACTTTAC 5672
QY 6339 CCTCAGATGAGTACTCTCTCAGGAGAAATGATGATTTGAATTTTATGAG 6398
Db 5673 GCTCTTTGTGAACTTTTCAAGTGAAGAAAGCAATTTGATGACTGGAAGTATTTATGG 5732
QY 6399 TCCATCAGGACAGAGTCTCTGCTGAAGCCCTCAGTGGGAATTACTCAGCTCCCTGAT 6458
Db 5733 TTTCTTGGGCAAAAGTCTTTGTAGTGTCTTAAGTGGGAACCACTGAACAGTCCA 5792
QY 6459 TGTCACTAGCTCAAGCACTCTGTGTACTGTGTGTGTCTGATCAAGCTTCAATCG 6518
Db 5793 TTTTACAGAGAAATGATCCTGATCTGATCTGCTGCTGCTCAAGATATGCAACAGAA 5852
QY 6519 GAAAGGCTTCAAAATCCGCTATTCAGCCCTTACTGAGCTGCGCAGGCTCCACTCCA 6578
Db 5853 GAAAGATTTCAAGATTTGCTATGCTAGCTCTTACTGAGCTCACTTCACTCAAGAA 5912
QY 6579 TGGCTTCACTCTGAGGACAGACAGACCCAGCCGGGGGCTCATCACTTTGGCTGCA 6638
Db 5913 TGGTGGCGTTTAAATAAACCGCAGCGCCCTGGGAGCAAGTGCAGATTTCTGCA 5972
QY 6639 CGCGGCTTACCGCTGTGTGGACACAGCATGGCTATCTGTACCGGCAACCCCAAGGCTTA 6698
Db 5973 GCTGTGATATCGAATATTTGGCACAAGAACGCACTGCAAGCGGAAACCACTGGGCGT 6032
QY 6699 CCACTGTGAGAGGAGGCAATCCCTCTCTGTCAAGCTTTCTGTGGCTCTCTCAAGC 6758
Db 6033 GATACAGTGGATTCATAGGCAACGCTTTGGCAGGCTGTCTGTGAAATTCAGAGG 6092
QY 6759 CCAAGAAATGATGATGTTTGGCAAGAGTACACAGTGGGAACCAAGGCGCTGTACAG 6818
Db 6093 TCCAGGAATGCTGTCTCAAGGCAATGATTTCACTTATGAAAGTAAAGTGACTTATGA 6152

QY 6819 CTGAGTGAAGGCTACCACTCCAGGACAGCGCTGAGGCCACTGCAAGTGTCTGACAC 6878
Db 6153 ATGTATATGAAGCTTCAAGCTGATGATGCCAGTGAAGCACTGCTGTGTCTCAAGAA 6212
QY 6879 AGGCTTATGAGCAACCGCAATGTCCACACAGTGTGTCTGTGACTTGTCTGATGT 6938
Db 6213 TGGCTGTGAGCAACAGAGAAAGCACCCAGTGAACCGGTGGCCCTGCCAGCAT 6272
QY 6939 CAGTACATCAGCGTGAAGCATGGCCGATGAGGCTTATCTTTGAGACACAGTATCAGT 6998
Db 6273 CGAAGCCAGCTGTGAGAGCAGTGTCTGAGGCTGTGTGTGGATATCTTAATGAATA 6332
QY 6999 CAGGCGCAGCTGATGCTCATGTGTGACCTGGCTACTATTACTGAGCAAGGCTCAT 7058
Db 6333 TGAAGCTCAAGTCTCTCAGCTGATGTCTGTGATCTTGTGAGGCTCAAGGCTGT 6392
QY 7059 CCGCTGTACAGCAATGGCAATGAGAGCTCGGGATCTTACGCCACCTGCGAATCAT 7118
Db 6393 GCAAGTCCAGCCATGGGACTTGGAACTGAGAGGACAGACCCAGATGTAAATGATCAT 6452
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Db 6453 CTCTGTGGAAGCTGTCTCTTCCCAATGTGAACAGATAGGAGCGCTCACTATGTA 6512
QY 7179 CGGGCAACAGCATCTTCTCCTGCAATTCGGGATTAACACTGAGGCTCCAGGGTGG 7238
Db 6513 TGAAGCACCGCATCTTCACTGCAATACCGGCTACACATTTGATGGCTCCATGTCCG 6572
QY 7239 TGAAGTATGAGCAATGGGCTCTGAGTGTCTGAAAGTCCGCTGCTGTGACATG 7298
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QY 7299 TGAAGCTCTGAGCCCATTTGTCAACGACATCAATGGGGAATCTACAGCTACCGGG 7358
Db 6633 TGGCTCTCAGAGCCCATTTGTGAATGGCCATATCAGTGCATGCTTCACTACAGGA 6692
QY 7359 CAGTGTGTATCAACATGCAATGATCTGGGCTCCGCTGATCGGATGTCTGAGCATCG 7418
Db 6693 CACAGTGTCTACCAATGCAACCTGGGTTTGTGACTCGTAGGACAGTGTGTAGAAATTTG 6752
QY 7419 CCAGAGATCATCACTGGTCCGGGACAGACCCCTTCTGTGTGCAATTTACCTGTGACA 7478
Db 6753 CTTGACAGACCAACAGTGTGTGGGACAGACCCCGTTTGTGCTCCCATCAATGTGGA 6812
QY 7479 CCAGGCAACCTGTCAACAGGCTCACTAGGATTAACAGTTTAACTTCAACAGTGTGT 7538
Db 6813 CCTGGAACCTGCCCCATGCTCACAACAGGAGCGATTCAACTGAATGACCTTGT 6872
QY 7539 CAAATTTGTTCGAACCTTGGGTATATGCTGAGGGGGGTGTAGTCCCATATGCTGTGC 7598
Db 6873 GAATTTTCACTTGCATACCGGCTTACCTGTGAGGGTGTCTCCAGGCCAAATGTGGAG 6932
QY 7599 CAGCGGCAATGAGTGAATCATGTGCCACTGCAAGAAATCATCACTGACATCTG 7658
Db 6933 CAAAGGCAAGTGAAGAGCCCTTGTCTATCTGCGAGTGTGAAGTGTCTCGATCTGG 6992
QY 7659 AACCAAGAAATAGTGTGTGTGATGATCCAGGCCAGCGGCGGCAAGGTTCACTTGG 7718
Db 6993 ATTTGTGAAATATGAGTGTGCTGCAAGGCAAGAACTTTCAAGAGATTTGAGATAG 7052
QY 7719 CACCACTGTGTCTTACCGGTGCAACAGGCTTTTAACTCTCTGGGCAACCCAGTGTCA 7778
Db 7053 GACAAATGTGATGTATCACTGCAAAAGGGGTTTAACTTACAGGCTCTTCTGCCCCG 7112
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Db 7113 CTGCAATGCAATGAGTGTGTGGAACCGCTCTTACCAAGTGTCTGAGTATCATGTGG 7172
QY 7839 CCAATCGGGCTCCCGCTCACTCCAGATGTCTGGAACAGTTTATCTGTGAGACAGT 7898
Db 7173 GCATCTGGGCTCCCGCTTAATGTGTCTGACTGGAAGAAATTTTACATTTGGAGCCAC 7232

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7233 AGTTAGATATCTCTCCAAAGGGGGCCAGATTCTCAAGGCATATACAGAGAGTCTGGCA 7292
7959 GCTGATGACACTGAGCTGGCTCCCTCCCTCACTGCTCAGGACCAAGCGTGGAGTTTG 8018
7233 AGAACAAGTCACTGAGAGTGAATCCCTTCCCATTTGTTCCAGAAATAGTCTGGATTTTGG 7352
8019 CGGTACCCCTGGGATCCCGGCTCATGGCATCGTTTGGGGGACAGCTTTGATCCAGGCAC 8078
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8139 TCAAGCCAAATGGCTGTGAGCGGCTCGACAGCTGAGTGTGAATCTTTTGGGAA 8198
7473 CTTGATGATGGGTCTGTGATCAGAGATCCAGCTGTGTGTGAGGCGGTCTGTGGAAA 7532
8139 CCTGGGATCTCAAGTAATGCCGAGTGTGTCTGATGA TGGCTGTTTCTCCAGCTC 8258
7533 CCTGGACACCTTACCAATGSSGATGATCTCTCAGACGATGGAATCTTCTCCAGCTC 7592
8259 TATCGTCTATGAGTCCGGGAGAGATATACCGCACAGGCTGTCTCAGCGCTCACTGCTC 8318
7593 TGTCTATATGCTGTCTGTGGAGGCTACAAAGACTCGGGGCTCATGACGGGCACTGAC 7652
8319 GGTCAATGATCTTGGACAGGCAATGACCTGAGTGTCTGTCAATPAACTGTGTGACCC 8378
7653 AGCGAAGGGAATGAGACAGGCAAGCCCTGATCTGTCAATCAATCAGTGTGTGATCC 7712
8379 TGGGATTCGAGCAATGGCTTCGCGTGGGCAATGATCAGTTCACAAACCTGTGAC 8438
7713 TGGCACATCTGCCAATGGCATCAAGTTTGGACAGACTTCACTTTCACAAACAGCTGAG 7772
8439 ATATCAGTGTATCCCTGCTATATATGATGAGTCAATAGATATCTGTGTGAGCTGAC 8498
7773 CTATCAGTGCACACCTGGCTTACTGATGAGGCCCAACATCAACCAACATCCGCTGAC 7832
8499 CAAGACCGGACATGAGATGGAACCAAGCCGCTGTGCAAAAGCTCTCATGTGCAAGCCAC 8558
7833 CAAGATGATCATGGAATCAGACCCGCGCTCTGCAAAAGCTGTCTATGACAGCAGAC 7892
8559 TCCGCTCATCCCAATGGGAGTGGTGGGCTGATCATTCATGGGGTCAAGTGTAC 8618
7893 TCCCTCAGTGCACAAACGAAAGTGGAGGGTCAAGCTTCGATGGGGTCCAGCATTAAG 7952
8619 TTATGCTGCTGAGAGGGTACCAAGCTTCCCTGCGCGGAGTGTCACTGTGAGGAGAA 8678
7953 CTACAGTTGTGTGATGGCTACCAAGTCTCCCACTGGGCATCTGTCTGTGAAAGGGGG 8012
8679 TGGGTCTGAGACCGAGAGCTGCTCAGTGTTCCTGTGTCTGCGGGGATCTGTGTGT 8738
8013 TGGAGTATGGAAGGAGAGTCCCTCAGTGTGTGTCTGTGTCTGTGTGTGTGTGTGTGT 8798
8739 CCGGTCCGTTGGAGAGAGAGACCGAGGCTTCTCTCAAGTGTGTGTGTGTGTGTGTGT 8798
8073 TCCAGAGAGGAGCGGCTCAGTGGGAAAGCTTCACTTTAAGTCTGAGGTCTTATCA 8132
8799 CTGCAATCCCTCTGT 8858
8133 GTGCAAAACCCATTTGT 8192
8859 ATGAGATGAGACCCAGCCGCTGATGATGATCCGACCTGACACAGTGTGTGTGTGTGTGT 8918
8193 GTGAGATGAGATCAGCCCACTGTGTATGATCCAGCCCAACCGGTTGGCCAGACCCGG 8252
8919 TGTGCAAGT 8978
8253 CACTCCCACTTTGT 8312
8979 CTTCCGTTGTCAAAAAGCTACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 9038

8133 CTTGAGATGTAGAAAAGTTTACCATATCAAGGCTCCACTACCGGACCTGTCTTGTCCAA 8372
9039 CCTGACCTGAGGTGGAACCCCACTGACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 9098
8373 CTTGACCTGAGGTGGAATTCAGACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 8432
9099 GCCAAGCATGCAAGCTGCGGGGCTGTGATTTTCCCTCATGTGGGCTTACAGCTCAT-TA 9157
8433 CCAAGCGATGCAATGTGAGAGCCATGATCTTCCAGCTTTTGTGTGTGTGTGTGTGTGT 8492
9158 CTCTGCGAGGAGGCTTCTCTCTCAAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 9217
8493 CACTGTGATCAGGATTTTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 8552
9218 TGGCAGCTGAGCAGGCAAGCCGCTCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 9277
8553 CATGAATGACAGGAAAGTCACTGTTT-----GTAAAGTAAAG 8594
9278 CAACACTGCGGGAGCCACCGCTCACCAAGCTTGTATCTGTGGGATGTTTTGTGCCAA 9337
8595 AGTGAAGAGATTAATGAACAGTTACTTAAACTCCAGTCTCTGTGTGTGTGTGTGTGT 8654
9338 GAATTCCTGTGAAAGGGGCTTATGAATACAGGGGAGAGAGAGCCAGCTGTGTGTGT 9397
8655 CAACCTCGGTGTGAAAGGATTAATGAATATTAGGCAAGAGACAGCGGAGCTGTGTGT 8714
9398 AGTACATGCTTCCAAAGTTGTCACAGCAAGTGTATGCCACATGATTCAGCAAGTGT 9457
8715 TGTGATCTGTTTAATGAACAGCAAGCAAGTGAATGACCTTCAACCGAGCTTCA 8774
9458 CGTGAAGCTGCACTTGTGTGAACTTCAAGAAAGAAATTTTATCTCTACTCTCAAGT 9517
8775 GTGTGAGTGTGAGCTGACAGGGGCTTCAAGAGAGAGAGGCGCACTGTGTGTGTGT 8834
9518 GTACCAATTAAGAGGCTGTGAGATCTTGTATGAATGATTCAAGATGATCACTGTGGC 9577
8835 CTTTCAATCAAAAGCCAGAGATTTTGTGAAGCAAGTTTAAATGACATCTGTGGG 8894
9578 TTTAGATGCGCATGCTGT 9637
8895 ACTGATGTGTATATCTGT 8954
9638 CAAGGCGCAAGCTTGTGGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 9697
8955 ACATGGAAGAACTTGTGGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 9008
9698 AGACCCGAGTGCATGTGCGGCACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 9757
9009 TGATGAGATTTCTTCAATCATATACAGGAGCAGCAGAGTGTGTGTGTGTGTGTGTGT 9068
9758 CTTGT 9817
9069 TCTGT 9128
9818 GAGAAGACCAAGTCTTCAATGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 9877
9129 AACAAAGCAAAAGTTCAATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 9188
9938 GCGGAGT 9984
9249 GTTGTGACAGCTGT 9295

RESULT 13
ADH72215
ID ADH72215 standard; DNA; 10989 BP.
XX
AC ADH72215;

XX 25-MAR-2004 (first entry)
 DT Human gene of the invention NOV54b SEQ ID NO:1111.
 XX
 DE da; gene; human; cytosolic; immunomodulator; neuroprotective; nootropic;
 XX anorectic; antidiabetic; antimicrobial; antilipemic; gene therapy;
 KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
 KW obesity; diabetes; infectious disease; metabolic syndrome X;
 KW dyslipidaemia.
 XX Homo sapiens.
 OS
 PN MO2003102155-A2.
 PD
 XX 11-DEC-2003.
 PF
 XX 03-JUN-2003; 2003WO-US017430.
 PR 03-JUN-2002; 2002US-0385120P.
 PR 04-JUN-2002; 2002US-0385784P.
 PR 05-JUN-2002; 2002US-0386041P.
 PR 06-JUN-2002; 2002US-0386047P.
 PR 06-JUN-2002; 2002US-0386376P.
 PR 06-JUN-2002; 2002US-0386453P.
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 PR 06-JUN-2002; 2002US-0387016P.
 PR 07-JUN-2002; 2002US-0387966P.
 PR 07-JUN-2002; 2002US-0386816P.
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 PR 07-JUN-2002; 2002US-0387262P.
 PR 08-JUN-2002; 2002US-0296960P.
 PR 10-JUN-2002; 2002US-0387400P.
 PR 10-JUN-2002; 2002US-0387535P.
 PR 11-JUN-2002; 2002US-0387610P.
 PR 11-JUN-2002; 2002US-0387625P.
 PR 11-JUN-2002; 2002US-0387634P.
 PR 11-JUN-2002; 2002US-0387688P.
 PR 11-JUN-2002; 2002US-0387696P.
 PR 11-JUN-2002; 2002US-0387702P.
 PR 11-JUN-2002; 2002US-0387836P.
 PR 11-JUN-2002; 2002US-0387859P.
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 PR 12-JUN-2002; 2002US-0387934P.
 PR 12-JUN-2002; 2002US-0387960P.
 PR 12-JUN-2002; 2002US-0388022P.
 PR 12-JUN-2002; 2002US-0388096P.
 PR 13-JUN-2002; 2002US-0389123P.
 PR 14-JUN-2002; 2002US-0389118P.
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 PR 14-JUN-2002; 2002US-0389146P.
 PR 17-JUN-2002; 2002US-0389729P.
 PR 17-JUN-2002; 2002US-0389742P.
 PR 18-JUN-2002; 2002US-0389844P.
 PR 19-JUN-2002; 2002US-0390066P.
 PR 19-JUN-2002; 2002US-0390209P.
 PR 21-JUN-2002; 2002US-0390763P.
 PR 17-JUL-2002; 2002US-0396766P.
 PR 06-AUG-2002; 2002US-0401628P.
 PR 09-AUG-2002; 2002US-0402156P.
 PR 09-AUG-2002; 2002US-0402256P.
 PR 09-AUG-2002; 2002US-0402389P.
 PR 12-AUG-2002; 2002US-0402786P.
 PR 12-AUG-2002; 2002US-0402816P.
 PR 12-AUG-2002; 2002US-0402821P.
 PR 12-AUG-2002; 2002US-0402832P.
 PR 13-AUG-2002; 2002US-0403448P.
 PR 13-AUG-2002; 2002US-0403459P.
 PR 13-AUG-2002; 2002US-0403531P.
 PR 13-AUG-2002; 2002US-0403532P.

PR 13-AUG-2002; 2002US-0403563P.
 PR 13-AUG-2002; 2002US-0406117P.
 PR 15-AUG-2002; 2002US-0406179P.
 PR 26-AUG-2002; 2002US-0406182P.
 PR 26-AUG-2002; 2002US-0406355P.
 PR 27-AUG-2002; 2002US-0406240P.
 PR 12-SEP-2002; 2002US-0410084P.
 PR 20-SEP-2002; 2002US-0412528P.
 PR 23-SEP-2002; 2002US-0412731P.
 PR 30-SEP-2002; 2002US-0414801P.
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 PR 30-SEP-2002; 2002US-0414840P.
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 PR 09-OCT-2002; 2002US-0417186P.
 PR 09-OCT-2002; 2002US-0417406P.
 PR 23-OCT-2002; 2002US-0420639P.
 PR 28-OCT-2002; 2002US-0421156P.
 PR 31-OCT-2002; 2002US-0422690P.
 PR 01-NOV-2002; 2002US-0423130P.
 PR 05-NOV-2002; 2002US-0423798P.
 PR 05-NOV-2002; 2002US-0423798P.
 PR 12-NOV-2002; 2002US-0425453P.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Alsbrook JP, Alvarez E, Anderson DW, Boidog FL, Casman SJ;
 PI Caterlon E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Elleman K;
 PI Eitenberg S, Gangoli EA, Gerlach VJ, Gorman L, Gunther E, Guo X;
 PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, MacDougall JR;
 PI Macschlian T, Malyanar UM, Mezick AJ, Mallet I, Mishra VS;
 PI Padigara M, Patirajan M, Pena CE, Peyman U, Raha D, Raselli L;
 PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shinkens RA;
 PI Smithson G, Spytek KA, Stone DJ, Vernet CM, Voss EZ, Zhong M;
 PI Zhong H;
 XX
 DR WPI; 2004-081935/08.
 DR P-PSDB; ADH72216.
 XX
 PT New NOVX polypeptides and nucleic acid molecules useful for preventing or
 PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
 PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
 XX
 PS Example 54: SEQ ID NO 1111; 1880bp; English.
 XX
 CC The invention relates to a novel isolated polypeptide (NOVX). A
 CC polypeptide of the invention has cytosolic, immunomodulator,
 CC neuroprotective, anorectic, antidiabetic, antimicrobial, and
 CC antilipemic activity, and may have a use in gene therapy, and as a
 CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
 CC any of the 303 fully defined nucleotide sequences given in the
 CC specification. The polypeptide is useful in the manufacture of a
 CC medicament for treating a syndrome associated with a human disease. The
 CC polypeptide, polynucleotide and antibody are useful in diagnosing,
 CC treating or preventing NOVX-associated disorder, e.g. cancer, cachexia,
 CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
 CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
 CC further used as hybridisation probes, in chromosome mapping, tissue
 CC typing, preventive medicine, and pharmacogenomics. The present sequence
 CC encodes a NOVX polypeptide of the invention.
 XX
 SQ Sequence 10989 BP; 2700 A; 2872 C; 2781 G; 2636 T; 0 U; 0 Other;
 XX
 QY Query Match 41.2%; Score 4174.2; DB 12; Length 10989;
 QY Best Local Similarity 64.8%; Pred. No. 0;
 QY Matches 6407; Conservative 0; Mismatches 3358; Indels 118; Gaps 10;
 Db
 QY 103 CTAGCTCAAGACCAATTGAGTGAAGTCTGAGGCTGAAGTCCGCAAGAC 162
 Db 1213 CAAGTGAAGGCGATTGAGTGAAGTGAAGGAGTCAAGTCTGCCGCAAGAT 1272
 QY 163 AACAGCCAGAAAGCGTGTGTTAACTCAGGTGTGTGTTCCCAAGACATAATGTGT 222
 Db 1273 GGAAGCCATTAATACTGTCTTGAGCCAGAGAGGTGTCATTGTCTCTCATGTGT 1332

QY 223 CCAAGCCCTGGGATACCCGAAAGGGGCAAAAGACTAGGCTCGATTCTC---AGTTAGGA 279
 DB 1333 CTAGATCTCGGGATTCAGAAAATGTGTGAAGAGAGGTTCCGACTTCAGTAGAGGTTGGT 1392
 QY 280 TCCAGCGTCCAGTTCACCTGCAACGAGGGCTATGACCTGCAAGGGTCCAGCGGATCAC 339
 DB 1393 GGAATGTACAGTTTTCATGTGAGGACAATTAAGTCTCCAGGAGATCTAAAGCATCAC 1452
 QY 340 TGTATGAAGTAGAGGACATGTTTTCGGGCTGAGACGACCAAGGGCGATGCGAGGCC 399
 DB 1453 TGTCAAGAGTTTACAGAGACGCTGCTGTGTGAGATGACACAGGCCATCTGCGAGCG 1512
 QY 400 CCGATGTGTGATGCCACCTTCGAGGGCCCTCGGGCATCATCACTCCCAATTTTCC 459
 DB 1513 AGAATCTGTGATCCAACTGTGTGGGGCCAGGGCGTCACTTCTCCCTTAATATCCG 1572
 QY 460 ATTCAATATGACAAATGACACATCTGTGTGTGATCATACAGCACTCAACCCCTCCAG 519
 DB 1573 GTTCAGATATGAAGATATATGACACATGTGTGTGATCATCACCAAGCCGAGCAAG 1632
 QY 520 GTGATCAAGCTCGCTTTGAGGAGTTGATTTGAGAGGGGCTATGACACCTGACGGTC 579
 DB 1633 GTCTATCAAGCTTGTCTTTGAAGATTGAGCTGAGCGAGGCTATGACACCTGACGGTT 1692
 QY 580 GGTGATGTGTGTCAAGATGAGGAGCCAGAAAGACATTTCTTACATGTCTCAAAATGCTGC 639
 DB 1693 GGTGATGTGTGGAAGGTGGGAGACACCATGCGTCTTGTACGTG----- 1737
 QY 640 AGTGAACAGCCCTACACCCCAAGGCTCTCCATCCCAAGAGAGATGTGGGACATGTGG 699
 DB 1738 -----CTCAGGGATCCAGTGTCTGACCTCAT--TGTGACATGAGC 1779
 QY 700 AGCGAATATGACTGTATCTTGAGATCTGTGTGATGACATTAGACATTCAGATSCAAGTCA 759
 DB 1780 AACCAATGTGTGTATCATCTGACGTGAGATGATGATGATGCT----- 1822
 QY 760 GGTTCAGTAGGAATCTCCAAAGACTTCTAATGTGTGTGAACTTGTGTCTCTGGGACA 819
 DB 1823 -----CACTGGGTTTAAACCTGTTTACCA 1848
 QY 820 GAGATGAGAGAGGAGAGTTCGAGTACCTGTGATACCTGTATGAGCGAGGAAAGGC 879
 DB 1849 GAATTTGAAAAGGAGGAGTGTGGGATCTGTGAATCCCGCTAATGGAAAGGAGCGGGC 1908
 QY 880 TCCCGGTTTACCAAGGTGACACATCTCAAGTTTGAAGTCCAGCCCGCTTTGAGCTGTG 939
 DB 1909 AGCAGTTTCTCCATGAGATACACTCACTTGAATGCCGCGCGCTTTGAGCTGTG 1968
 QY 940 GGAAGAAAGCAATCAATGTCCAAAGATTAACCAATGTGCGCTAAGAAAGCAGGCTGC 999
 DB 1969 GGGAGAGAGATTATCACCTGTGACGACAAATCATGTGTGTGACCAAGAGCCACTGT 2028
 QY 1000 GTGTCTCTGCTCTTCTCAACTTTCACAGGCCGCTGTGGGTTGTCTGTCTCCCACTAC 1059
 DB 2029 GTATTTTCAHTTTCTTCACTTTAAGGCATCACTGTGGATTAATCTGTACCAAAATTAAT 2088
 QY 1060 CCAAGAGACTATGGCAACCACTTCATGTGTCTGTGCTCATCTGTGCGCAGGCGTGAAGC 1119
 DB 2089 CCAGAGGAATATGGGAAACAAATGACATGATGTGTGTGATTAATCTGTGAGGCAAGAGT 2148
 QY 1120 CGCATCCAGCTGGGCTTCAAGCAATTTGACGTGAGCCTCAGTTTGAATTTCTGTGTATC 1179
 DB 2149 CGAATTCACCTAATCTTTAATGATTTTGAATGTGAGCTCAATTTGACTTTCTCGGGCT 2208
 QY 1180 AAGATGGGGCCACCGCGAGCGCGCTCTGTGGCACCTTCTGAGAAACAGCTTCC 1239
 DB 2209 AAGATTAATGGCATTTCTGACATACTGTCTGTGGTACTTTTCTGTGCAATGAGTCCCT 2268
 QY 1240 TCTCTCATCAAGAGAGTGGCAGTGGCCGCTCTGAGTTCAGAGTTCAGACCACTCCACA 1299
 DB 2269 TCCAGCTGGCCAGAGAGTGGCATATGATGTGCTTGTGAATTTCAAGTCTGACATTTCCACT 2328

QY 1300 GGAAGAGGGGCTTCAATCATCTTTTCAACTTCCAGACAAAGATGCGCGGATCT 1359
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 QY 1360 GCGGTTCCAGATAATGGCAAAAGGTTTGGGAGACAGCTTCAGCTGGGCACTCCATCTCC 1419
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 QY 1540 CACCTGACTTGTGCGCCAGCGGACATCTCTCTCGGGCTGTGGCTGTGTGTGTGTGTGTGT 1599
 DB 2569 CATCTGACAGCGTCCAGCGGAGTCAATTTTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGT 2628
 QY 1600 GCTTGAAGCTGTGCTGGGATGATGAGGCCAGCGCTACCCCAATCAAAATCACTTTC 1659
 DB 2629 TCTTACATTTGATATGATATTTGAAGCAAAACAGCCACTTATCAAAATGACTTTT 2688
 QY 1660 GACAGATTCAAAACGAGGTCAATATGACACCTGGAAGTACGATGCGGCGGACTTAC 1719
 DB 2689 GAGAGATTTCAGACAGAGGTCATTTATGACACTTGAAGTCAAGATGAGGCGCAGCACT 2748
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 DB 2749 TCGTCCCACTGTATGCGCGAGTACAGGACCCAGGACCCCAAGTTCTTCACTAGACAC 2808
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 DB 2809 GGAATCTTCAATGATACCTGCTGTTCACACATGACAGACCGGCTTCAGACATCGGCTTCTC 2868
 QY 1840 CTTCGCTATGAGACTATATACATCTGACGTCAAGACCACTGTGTGATCCAGAAATCCAGTA 1899
 DB 2869 ATCCACTATGAGATGTGAGCGTGTGATTCGATTCCTGTGTGAGCCGCGCATCTCTGTG 2928
 QY 1900 AATGACAGCGTCAATGGAATATGACTTCTACGTGGCGCGCTGTGTGACTTCACTGTGAC 1959
 DB 2929 AACGCACTGTGCGAGGTGAGACTTGTGATCAGTTCACAGTATTTCACTGTGTGAC 2988
 QY 1960 TCGGCTTACATTAATGAGAGGAGCCTGTGAGTGTGAGCCCACTTCCAGTGTGAGC 2019
 DB 2989 CCGGGATACACATTAAGTACAGAGACCCCTGTGTGTGAGAGAAACACACATGTGAGC 3048
 QY 2020 CGGGCTTGTGAGTGTGAGTCTCTGTGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 2079
 DB 3049 CACGCTTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 3108
 QY 2080 ATCTTGTGAGGAGTTCCTGTGACTTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 2139
 DB 3109 GTCTTGTCTCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 3168
 QY 2140 GAATATCTATGAGAGGAGTGTGTCTTCACTTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 2199
 DB 3169 GAATGTCTCATGGAAGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 3228
 QY 2200 CATGACTATCTCTCATATGAGAGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 2259
 DB 3229 CAGCACTTATTAATGATATCAAGAGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 3288
 QY 2260 GATATCGGCTGCGCACTTCCATACAGCGTGGGCTGTATGAGCAATCTTCACTGTGAGTGTGAGTGTG 2319
 DB 3289 GGT 3348
 QY 2320 GCTTCTATCTGT 2379
 DB 3349 CGATTATATCAAGACTTCTCAATTTGTGAGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 3408
 QY 2380 GACTTGTGAGCCTGTGAGAGAGCCGAGGTCCAGGCTTCAAGATTCGGAAGGAGGCTTGTGAG 2439

Db 3409 GACCTGGAGCAGTGTATGATCTCGAGTCCCTGCTTACGCCGAGAAATGGTTTTTCAC 3468
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Db 3469 TTTGGTGGGAACTCTCGACGTTTTCTGCTCTCTGGATATGTTTTAGAAAGGTGCG 3528
Qy 2500 GCCCGCATCAGTGGCTGGGGGGGAGAGCGGCGCTGGAGCTGGGCTCGGCAAGGTG 2559
Db 3529 ACCAAGCTTACCTGGCTGGGGGGGGCGCGCTGTGTGAGTCACTCTGCGCAAGGTG 3588
Qy 2560 GTTGTGAGTGGGGAATTCAGTACAGAGCACTCAGGGTACTTGTGTCCCAACTT 2619
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Qy 3040 GGAGAGCGCGGACCTGGGACCGGCGCTGCGCAACCTGTGTGGCGAGTGGAGGACA 3099
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Qy 3100 GTGAGAGAGAGGTGTGGGGGAGTGTCTGACCCGGGATCCAGCTCCCTATGAAC 3159
Db 4129 ATCCATGCAAGCCATCAGAGCAATATTTCTCCCTGGCTATCCAGCTCCGATGACAC 4188
Qy 3160 AATTCATCTGATCTGACATCAGACAGAGAGCGGCTGACCAATTTGGGCTACATTC 3219
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Qy 3220 CTGGTATTGACACAGAGAGTTTCAAGCTGTGCGATCTTGGGATGGGCTGTGAG 3279
Db 4249 ATTTGTTTGACACGAGATGTGCTCAGACATCTTAAGGTCTGGGACGGGCGGTGAC 4308
Qy 3280 AGCGGGTTCTGTGAGAGAGTGTGGCCGGGCTGGCCCAAGACCTGCAATGACAC 3339
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Qy 3340 TTCAATCTCGTGTCTGTGACATTCAGACTTCTTTCACAGCAAGAGGCTTTGCC 3399
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Qy 3520 TACGGCTGACAGGAAGTGCAGAGATCACTGTGTGAAGATGAGAAACAGTTCTTCTGG 3579
Db 4549 TATCAGCTCCAAAGACAAACCAAAATCACTGTGTGACGTAATAACGCTTCTTTGG 4608
Qy 3580 CAGCCAGCGCGCAACATGATCGCTCCCTCGGGGAGACCTGACAGAACCATCTGGA 3639
Db 4609 CAACAGACCTCTCAATGATGATAGCTGTTGTGAGAGGAATGTGACGGGCCAGAGGT 4668
Qy 3640 GTATCTCTCAACCAATTAACCAAGACCTTACCCGCAAGGAGAGTGTGATGAGAA 3699
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Qy 4180 TACCCCAAGATCAACAGTGAACAGATCTGCTGTATTTTGTATCTGTGCCAAGAC 4239
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Qy 4300 CAGCAGGCAAGCAGACACTGGGGCTCTCAGCTCCCTGCGGGCTCCCATACAGA 4359
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Qy 4360 GAATCACTGCTTGGCCACTTCAATCAATCAATTTTCAATTTAGTTCAGCCCAAGGCTTC 4419
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Qy 4420 GCAACAGCAGAGGCTTCACTTTGTCTTCAAGAGGTTCTGGAACAGCGCCAGCGAG 4479
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Qy 4480 TGAAGCTGTGCGCGAACCCTGATATGCAAGAGGCTGGAGTCACTTCTCGGTGGG 4539
Db 5509 TGAAGCTGTGCTCCGAGCCGAGATACGAAAGAAATTTGTTCTGAGTTTCTGCGGCG 5568
Qy 4540 GCCATGTCGCTTCAATGCAATCTCGGCTATGCTCTGCAAGAGGTGCGCAGAGATCGAG 4599
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QY 4660 CCGTGTGAGGCAACCTCCAGAGCGGAGGCAACATCTGTCCCTGTGCTCCCAAG 4719
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QY 4720 CCGTACCTTACAGCCTCAACTGTGTGTGAAGATGTGTCTCCGAAGGGCTGGCA-T 4778
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QY 4779 CCAAGTCCAGTTGTGAGTTTGTGACAGAGCAACTGGGACT--CGGTGAGATATT 4836
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QY 5017 GTGCCAGATACCGGGGTGAAGACTGGCGAGCGCTACTTGTGAATGATGTGTCTTTC 5076
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QY 5257 TGTCTGTGAAATPACACTGCCCCGTGGGCTTGGAGTCACTCCAGTCTCTGAATTC 5316
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QY 5377 ATGATGGGAATTCAGTGAACGAGCTTCCAGCTCCCTCTCTCCAGTCCCAAG 5436
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QY 5437 ACCACGTGTATTTCAACAGGACCACTCCCAAGATCGGCAAGGATTCAGCTGAGTAT 5496
DB 6469 ACCCTATCCACTTTATATGTGACATTTGCAAAACCGGCAAGATTTAACTTGTCTTAC 6528
QY 5497 CAGGCTATGAACTTCAAGAGTCCCAAGCCAGACCCCTTGGCCAAATGGCATTTGTAG 5556
DB 6529 CAGGCTATGAAATTTACAGAACTGTCCAGATCCACCCCAATTTGAGAAATGGGATCATGATC 6588
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QY 5617 ACTGGCAACCTGTCTCTCAAGTGAACAGTGAACCAACGGGAACCTGGGACCAACCCCTG 6676
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QY 5677 CCAAGTGTGAGTCCCTGTGTGGCGGGAACATCACTTCTTCAACGCACTGTGTACTCC 5736
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QY 5737 CCGGGGTTCCCTTACCCGTACTCAGCTCCAGAGATGTGTCTGTGATCAACCGTCCC 5796
DB 6769 CTTGGCTTTCTTATGATGTATCCGATCTGGAAGAGATGCAATTTGGCTCATACGGTCTT 6828
QY 5797 ATTGGCCATGGCGCTCCCACTCAGCTCTGTGAGACAGAGCCCTGTGAGATTTTC 5856
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QY 5917 ATGGCCAAAGAAACAGTGCAGAGTTCACTCAACAGGTCTGTCTCAAGTTTCCACCGAT 5976
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QY 5977 GCAAGCCAGAGGGGATCTTCCGCAATAGCTTCTCGCTTATCCACTCACCAATGCTCT 6036
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QY 6037 CTTCCCAACATCTTCCCAACGCGGAAGTGTCAACAGAAATGAATATATAGT 6096
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QY 6157 TGCAAACTTGGAACTTCTGAGTTTGAAGACCAACCCCGATATGTAAGTGTGACTGT 6216
DB 7189 TGCAGCTCAGTTTCCAGTGTGAGTTGAGGGTTCTTCCCAACATGTGAAGCAATATC 7248
QY 6217 CCAACAAATGACTTCTGACAGATCTCAACAGGCTGATCTGTAGCCAGAGTACCTTGA 6276
DB 7249 CCAGCAATGAAATCCCGAGCTGATCATCGGAGTCAATTTCTCAGTCCAGGGTATCCGGGT 7308
QY 6277 AGCTATCCCACTTCCAGACCTGTCTGTGGTGTGAGTGAAGGCCCACTATATATC 6336
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DB 7369 ACATCTTTGTGACACATTTCAAAATGAAAGAGTTTGTGACATGGAATGTTGAT 7428
QY 6397 GGTCAATCAGACAGATCTCTGTGAAAGCCCTCAGTGGGAATTTACTCAGTCCCTG 6456
DB 7429 GGTCTTCTGGCAAGTCTCTGTGTATGTCTTAAGTGGGAATCATCTGAACATCA 7488
QY 6457 ATTGTACACAGCTAAGCACTGTGTGACCTGTGGTGTGATCTGATCAAGCTTACAT 6516
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QY 6517 CGAAGGGCTTCAAGATCCGCTATTCAGCCCTTATGACAGCTTGGCCAGGGCTTCACTC 6576
DB 7549 AAGAAAGATTCAGATTCGCTATGACAGCACTTACAGTGTGACCAACCCCTGAAG 7608
QY 6577 CATGCTTATCTTATAGGCAACAGACCCAGCCCGGGGCTCAATCATTGGCTGC 6636
DB 7609 AATGGGGATTTCTTAAACAGAGCTGACAGAGCGGTGTGAACCAAGTGCATTAATTTTGC 7668
QY 6637 AACGGGCTACCGCTGTGGGACACAGATGAGCAATCTGTACCCGGACCCCAAGGCG 6696
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QY 6697 TACCACTGTGAGGAGGAAGCATCTCTGTGTGAGCTCTTCTGTGTGGCTTCTGAG 6756
DB 7729 ATGTACAGTGGAGATCCCTCAGCCCACTGTGCAAGGCTGTGTCTGTGGAATCCAGAA 7788
QY 6757 GCCCCCAAGAAATGGAATGTGTGTGGCAAGAGTACACAGTGGGAACCAAGCGGTGTAC 6816

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Db      7789  TCCCCGAGAAACGGTTCATTACCGGGAGACAGTTCATCTTGGACAGTAAAGGTCTAT 7848
Qy      6817  AGCTGAGTGAAGGCTACCACTCCAGGAGGGGCTGAGGCCACTCAGAGTGTGAC 6876
Db      7849  GAATGTCATGAAAGGCTTCAAGCTTGAATCCAGCCAGACAAACAGCCGTGTCAAGAA 7908
Qy      6877  ACAGGCTTATGAGCAACCGCAATGTCCCAACAGTGTGCTCTGTGACTTGTCTGTAT 6936
Db      7909  GATGGGCTGTGAGTAAACAAGGGGAAGCCGCCATGTGTAGCCGGTCCGTTCCAGC 7968
Qy      6937  GTCAATGACATCAGCGTGAAGATGGCCGATGAGGCTTATCTTTGAGACAGATCAG 6996
Db      7969  ATTGAAGCTCAGCTCAGAACATGTCACTGAGAGCGTGTTCAGGATCTTGAATGAG 8028
Qy      6997  TTCAGAGCCCAAGTATGTCTCATCTGTGACCCCTGGCTACTACTATCTAGCCAAAGGTC 7056
Db      8029  TACGGTCTCAAGTATTTGCTGAGCTCAGTCTGTGTACTTATAGAAAGCTGGAGGCTC 8088
Qy      7057  ATCCGCTGTCAAGGCAATGAGCAATGAGGCTCGGGGACTCTAGCCCACTGCGGATC 7116
Db      8089  CTGCGGTCCAGGCCAATGGGAGCTGGAACTAGAGATGAGAGGCCAAGCTGTCCAGTT 8148
Qy      7117  ATCTCGTGAAGAGCTCCCGATTTCCCAATGGCCACCGCATCCGAACTGTCTGTCTC 7176
Db      8149  ATCTCGTGAAGAGCTTCTCTTCCCAATGGCAACAAATGGAAGCTTGACAGTT 8208
Qy      7177  TACGGGGCAACAGCCATCTTCTCTGTCAATCCGGAATACACATGTGTGGCTCAGGGTG 7236
Db      8209  TATGGGGCCACACCTATATTTACGTGCAACACGGGCTACACGCTTTGGGGGTCTCATGTC 8268
Qy      7237  CGTGAATGACATGAGCAATGGGCTCTGGAAGTGGCTCTGAGTCCGCTGTGTGACAC 7296
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Qy      7297  TGTGGAGCTCTGAGGCCATTTGTCAACGACATCATATGGGAGAACTACAGCTTACCGG 7356
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Qy      7357  GGGAGTGTGTATCCAAATGCAATGCTGCTTCCGCTGATCGGCAATGTCTGTGCGCATC 7416
Db      8389  GACACGTGTATTAACAAGTGCATCTGTGTTTCCGGCTGTGGGAATTCCTCGAGAGAA 8448
Qy      7417  TGGCAGAGGATCATCATGAGTGGGGAAGACCCCTTCTGTGTGCAATTAACCTGTGGA 7476
Db      8449  TGGCTTCAAGAACCAAGTGTGTGGAACAAACCGCTGTGTGCTGTATCAATGTGTG 8508
Qy      7477  CACCCAGGCAACCTGTCAACGAGCTCACTCAGGGTAAACAGTTTAACTCAACGATGTG 7536
Db      8509  CACCTTGGAAACCTTCCCAAGGATTCATTAATGCAATGATTTCAACTGAAATGATGTC 8568
Qy      7537  GTCAATGTTGTTTGAACCTTGGGTATATGCTGAGGGGGCTGTAGTCTCCAAATGCTG 7596
Db      8569  GTGAATTTTCACTGCAACACGGGCTATTGTGCTCAGGGGCTGTCTGAGGCCAGTGTG 8628
Qy      7597  GCCAGGGGGAATGAGTGAATGCTGCCCCAAGTGTGAGATATCAATGTATACAGATCTC 7656
Db      8629  AGCAAGGGCCAGTGAAGTACCTCTGCCCCAGTGTGAGTGTGAACTGTGTATCA 8688
Qy      7657  GGAACAAGAAATAGTGTTCGTCAAGTCAACGAGCGGCGGCAAGGTTCAAGTTCC 7716
Db      8689  GGCTTTGTGGAATAATCCATTCGTCAAGGCAACAAATCTTCCCTGAGAGTTTGTAGAT 8748
Qy      7717  GGCACACTGTGTCTTACCGGTGCAACAGGCTTCTACTCTGTGGGCAACCCAGTGTCTC 7776
Db      8749  GGAATAGATCTCTGTACATTCAGAAAGGGAATTTACTGTGTGGATCTTCAAGCTTGC 8808
Qy      7777  AGCTGACAGGAGATGAGCAATGGGACCGTCCCGGCCCCAGTGTCTTGTGTGTCTGT 7836
Db      8809  ACTGTATGCAATATGCTTATGGAGCCATCTTCCCAAGTGTGTGTATATGTGT 8868
Qy      7837  GGCATCCGGGCTCCCGGCTCACTCCAGATGTCTGAGACAGTTATCTGTGGAGCA 7896

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Qy      7897  GTGTGCGGATCAGGCTCATTCGCAAGCGTACTGTGTGGGAAACGACCCGATGTGT 7956
Db      8929  GTCTGTACTTACTCTCTGCAAGAGGACGAGAGCTTCATATGCGACACAGAGTGTG 8988
Qy      7957  GGGCTGTATGACACTGGAATGCTCTCCCTCCCTCACTGCTCAGGAACAGCGTGGAGTT 8016
Db      8989  CAGAAAGACATGCACTGAGACGGGGGCACTGCCCACTGCAAGAAATATCTGTGATTC 9048
Qy      8017  TGGGTGACCTCTGGGATCCCGGCTCAATGAGCATCCGTTGGGGACAGCTTTGATCCAGC 8076
Db      9049  TGTGTGATCCGGGGGACCCACACATGAGTGTCTGGCTTGTGTATGACTTTAAGCAAG 9108
Qy      8077  ACTGTATGCGGCTTCACTGTGAAGCTGGGCAAGTCTCCGGGGAATCTGACAGCGCAC 8136
Db      9109  AGCTTCTCCGCTTCTCTGTGAATGGGGACACAGTGAAGGGCTCCCTGAACGACAG 9168
Qy      8137  TGTCAAGCCAAATGAGCTCGTGAAGCGGCTGCAAGCTGAGTGTGAGTATCTTGTGGG 8196
Db      9169  TGTGTGTCAATGGGTCATGTCAGGACCTGAGGCTGTGTGAGCCGCTGTCTGTGGC 9228
Qy      8197  AACCTGGGACTTCAAGTATATCCGAGTGTGTGTCAATGATGAGTGTGCTGTCTCCAGC 8256
Db      9229  AACCTGGGACACCCACCAAGGAATGATGTGACATGATGAGTGTGAGTGTCTGTCTCAGC 9288
Qy      8257  TCTATCGTATATGAGTCCGGGAAGGATCTAAGCCACAGGCTGTGACCCGTCACTGC 8316
Db      9289  TGGGTATCTATGCTCTGTGGAAGGCTAACAGACTCAGGGCTCATGACAGGCAATTC 9348
Qy      8317  TGGGTCAATGTATACCTGACAGGAGTGAACCTGAGTGCCTGTCTAATACTGTGTGAC 8376
Db      9349  AAGCCAAATGGGACCTGGAACAGGACATGCTCCCGACTGACAGATTAAGTTGTGGGAT 9408
Qy      8377  CCTGGATTCACCAATGAGGCTTGGCTGGGCAATGACTTCAAGGTAACAACAACCTGTG 8436
Db      9409  CCAGGACACTAGCAAAATGGCATCCAGTTTGGGACCGACTTCAACAAAGACTGTG 9468
Qy      8437  ACATATCAGTGTGCTCCCTGGCTATATGATGAGTGCATATAGATATCTGTGTGAGCTGC 8496
Db      9469  AGCTATCAGTGTATCCCAAGGCTATGTCAATGAGAGTGCATATCCGCACTATTCGCTGT 9528
Qy      8497  ACCAAGGACCGGACATGGAATGGAACCAAGCCGCTGTGCAAGGCTCTCATGTGCAAGCA 8556
Db      9529  ACCAAGGACCGGAGTGAATCCGACAAACCTGTCTGAAAGCCGTGTGTCTCTCAG 9588
Qy      9589  CCGCGCGGCTCAGATGGAACATGAGGGAAGTATTCGCGTGGGGCTCCAGCATAT 9648
Db      8617  ACTTATGCTGCTGTGAGGGGTAACAGCTTCTCCCTGCGCGGCTTCACTGTGAGGA 8676
Qy      9649  AGTTACAGCTGATGAGACGTTTACAGAGCTCTGCACTCCGCAATCTCTCTGTGAAAGT 9708
Db      8677  AATGGGCTCTGACCGGAGAGGCTGAGTGTTCCTGTTCCGTGCTGCGGGATCCTGTGT 8736
Qy      9709  CCGGGGTGTGAAGAGAGATCCCAAGTGTCTGCTGTGTGCTGTGCGGAACCTGTGC 9768
Db      8737  GTCCGCTCCCTGTGGAAGAGAGAGACAGAGCTTCTCCTACAGGTCATCTGTCTCTTC 8796
Qy      8797  TCTGTGATCCCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 8856
Db      9829  CAGTGAATCTTCAATTTATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 9888
Qy      8857  ACATGAGTGGACCAAGCCAGCTGCAAT---AGATCCGACCTGACCAAGTGTGTGTGT 8913
Db      9889  AGTGAAGGGAATACAACTCCTGCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 9948
Qy      8914  CCTGTGTGCAACAGTTTGGGATACGAACAATTTCTCAGGGGCTACAGGTTGGAAGCA 8973
Db      9949  CCTGTGTGCAACAGTTTGGGATACGAATACCTCAAGAGGCTTATGAGGTTGGAAGCAG 10008

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OY 8974 GTCTCTTCCTGTTGCAAAAAGCTACCTGCTCAGGGGCTCCACCACGAGACCTGCTC 9033
DB 10009 GTTTTTCAGGTGAGAAAAGCTACCTATTCAGGTTCCAGACTCGACCTGCTT 10068
OY 9034 CCAAACTGAGTGGAGAAACCCCACTGCTGTGCTCCACCACTGACGAGCCCA 9093
DB 10069 GCCAATTTAACTGAGTGGAGTACAGACCGAATGATATGTCATGCTCCGACAGACCA 10128
OY 9094 GAGAGCCCAAGCAAGTCCGAGGCGCTGGATTTGCTCCATGGGCTACAGCTC 9153
DB 10129 GAAACCCCGGACACGCGGATGTAGAGCATGCTCTTCACTTTCGGCTACCTTA 10188
OY 9154 AT-TACTCTGCGCAGAGGGGCTTCTCCCTCAAGGGTGGCTCCGACACCGCACTGCAAG 9212
DB 10189 GTGTACCTGCTCATTCAGGCTTTTCTCCGAGGGGATCTGACACAGAACTGTAA 10248
OY 9213 GCGGATGGCAGCTGACAGGCAAGCCGCAATCTGCTGGAGGTCGCGCCACGTGGAGA 9272
DB 10249 GCAGACATGAATGACAGGAAAGTCGCTGTGT-----GTAAAGT 10280
OY 9273 CCCATCAACACTGCCCGGAGGCCACCGCTCACCAAGCTTATCTTGGGAGTGTCTT 9332
DB 10291 AAAAGATGAGAAAGTTATGAAACAGTTACTAAACTCCAGTTCTTCAATGTCTTT 10350
OY 9333 GCCAAGATTCCCTGTGAAAGGGGCTATGAATACAGGGGAGAAAGACGACGACCAATG 9392
DB 10351 TTCTGCAATTACTGTGAAAGGGGTATTTGAAATTTTAGGAAAAAGAACACCCGCTACT 10410
OY 9393 CTCAGATGACTGGCTTCCAGTTGCAACAGCAAGTCAATGATCCACATGATGACAC 9452
DB 10411 CTAACTGTGATGGTTCAATCAACAGCAAGTAAAGTCAACCTTCAGCGAAGCC 10470
OY 9453 AGTGCGTGAGACTGCACTTGGCTGGAATTTACAAAGAAAGATTTTCACTCTTACTC 9512
DB 10471 TCGCAGTGAGAGCTGAAGTTGACAGGCAATTTCAGAAAGAGAGGCCCTACTTCTCTG 10530
OY 9513 CAGGTGATCAAGATTACAGGGGCTGTGAGATCTTATTAATTAAGTTCAAGATGATAC 9572
DB 10531 AAAGCTTTCAATTAAGGCCAGGCAAGATTTTTTTGTAAGCAAGTTCGAAATGACAAC 10590
OY 9573 TGGGCTTATGATGGCCATGTCTGTGAGAGTCTCCGAGCCACCTTCACTACCAAGGC 9632
DB 10591 TGGGAGCTAGATGTTATGTGTCACTGTGACTTGAAGAGGAGATTTTCACTTTCAAGGT 10650
OY 9633 TGTGTCAAGGGGCAAGGCTTTGGGAGCTTCCGCTTCAAGATCTGAGCTCAGCTGCTG 9692
DB 10651 GACATTTCAAGAAAAGACTTTGAAAATTTAAAGTAAAGGCAAGA-----TCTTTTA 10704
OY 9693 GAGTCAGACCCCGAGTCCATTTGCGCGCACTTTGCTTCCACAGACGCTCAGTGGCAGCC 9752
DB 10705 AACCCAGATCAAGACTCTTCCAGTCAATTCACAGGACACAGAGAGTGGCTCTGTGGCGCT 10764
OY 9753 GCGATCTGTGTCCTTTTCATGCGCCCTCATTTATGCGGGGCTGTGCTCTATCTTACAG 9812
DB 10765 GCCATTTGCTGTTCTTTCTCTCTAATTTATCAGGGTGTGCAATTTTACTCTTACAAA 10824
OY 9813 CACAGAGAAAGCCCAAGTCTTTTCATATGCTATGCTGCGCAAGAAACCAATGTT 9872
DB 10825 CACAGAAACAGACCAAAAGTTAAATCAATGCTATGCTGCGCAAGAAACGCAATGGA 10884
OY 9873 CCGGCGCATTTGAGAAACCAATGTACAGCCCAACATCCAGCCACAGACATCTATGGCC 9932
DB 10885 CAAAGCATCTTTGAAAACCCCATGTATGATACAACTTAAACCCACAGAACGCAAGCT 10944
OY 9933 AGCGAGCGGAGTCACTGACAGCACTGTGCAAGCAAGAT 9975
DB 10945 GTGAGGTTTGACACAACTCTGAACACAGTCTGTACAGTGTAT 10987

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RESULT 14
AAD33320
ID AAD33320 standard; cDNA; 10433 BP.

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XX AC AAD33320;
XX DT 01-JUL-2002 (first entry)
XX DE Human C3b/C4b complement receptor like cDNA #2.
XX KW Human; C3b/C4b complement receptor-like molecule; immune system disorder;
XX KW gene therapy; rheumatoid arthritis; psoriatic arthritis; osteoarthritis;
XX KW inflammatory arthritis; inflammatory joint disease; Alzheimer's disease;
XX KW multiple sclerosis; inflammatory bowel disease; nervous system disorder;
XX KW transplant rejection; autoimmune disease; ischemic condition; neutropenic;
XX KW metabolic disorder; immunomodulatory; neuroprotective; diabetes; lupus;
XX KW infertility; vasodilator; obesity; cardiant; gene; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT 1..9303
XX FT CDS
XX FT /product= "Human C3b/C4b complement receptor like protein
XX FT #2"
XX FT /note= "CDS does not include start codon"
XX FT /transl_except= (pos:2176..2178, aa:Xaa)
XX FT /note= "This translational exception occurs while
XX FT decoding the alternative version of human C3b/C4b
XX FT complement receptor like protein #2 (AAE20901)"
XX FT /partial
XX PN W02002010199-A2.
XX PD 07-FEB-2002.
XX PE 24-JUL-2001; 2001WO-US023232.
XX PR 02-AUG-2000; 2000US-0222504P.
XX PR 28-NOV-2000; 2000US-00728787.
XX PA (AMGE-) AMGEN INC.
XX PI Welcher AA, Eliott GS;
XX DR WPI; 2002-303934/34.
XX DR P-PSDB; AAE20789, AAE20901.
XX PT Nucleic acid encoding a novel C3b/C4b Complement Receptor-like nucleic
XX PT acid molecule, useful for treating, preventing and diagnosing rheumatoid
XX PT arthritis, psoriatic arthritis, inflammatory arthritis, and multiple
XX PT sclerosis.
XX PS Claim 1; Fig 2; 251pp; English.
XX CC The invention relates to a nucleic acid encoding a novel C3b/C4b
XX CC complement receptor (CR)-like nucleic acid molecule. The C3b/C4b CR-like
XX CC polypeptide and nucleic acid molecules may be used to treat, prevent,
XX CC ameliorate, diagnose and/or detect diseases such as immune system
XX CC disorders such as rheumatoid arthritis, psoriatic arthritis, inflammatory
XX CC arthritis, osteoarthritis, inflammatory joint disease, autoimmune
XX CC disease, multiple sclerosis, lupus, inflammatory bowel disease,
XX CC transplant rejection, nervous system disorders (e.g. Alzheimer's
XX CC disease), ischemic conditions, metabolic disorders (e.g. obesity and
XX CC diabetes) and infertility. The invention is useful in gene therapy. The
XX CC present sequence is human C3b/C4b complement receptor like cDNA
XX SQ Sequence 10433 BP; 2618 A; 2671 C; 2527 G; 2610 T; 0 U; 7 Other;
OY Query Match 40.1%; Score 4067.4; DB 6; Length 10433;
OY Best Local Similarity 65.5%; Pred. No. 0;
OY Matches 6001; Conservative 5; Mismatches 3136; Indels 25; Gaps 3;
DB 819 AGAGATCGAGCAGGCGAGTTCGGTACCTGCGCATACCTGCAATATGCGCGGAGGAAAG 878
DB 168 AGAATTTGAAAAGGAGGAGTGTGGGATCTCGAATCCCGCTATGGGAAGCGAGCGG 227

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QY	879	TTCCCGGTTTACCA	CGGTGACAC	CTGAAGTTTGAAGTGCAGCCCGGCTTTGAGCTGGT	938
Db	228	CAGCAGTTTCTCC	ATGAGATAC	CTCACTTTGAATGCCCGGGGCGCTTTGAGCTGGT	287
QY	939	GGGACGAGAAGGC	AATCAGATG	CCAAAMAATAAACAATGTCGGCTTAAGAACAGAGCTG	998
Db	288	GGGGGAGAGATT	TACCTGT	CAGCAGAAACAATGAGTGTCTGGCAACAAAGCCAGCTG	347
QY	999	CGTGTCTTCCTG	CTTTCACTT	CAAGCCCGTCTGGGGTGTCTGTCTCCCACTA	1058
Db	348	TGTATTTTCA	TGTTTCTTCA	ACTTTACGGCACAATCTGGGATTTATTTCTGTCAACCAATTA	407
QY	1059	CCGACGAGACTAT	GGAACCA	CCCTCACTGATGCTGGGCTCAATCCGCGCAGAGCCGTGAGAG	1118
Db	408	TTCAGAGGAAAT	ATGAGAAACA	CATTAACGTGTCTGGTTGATTTCTTGAGCCAGAGAG	467
QY	1119	CCGATCCACCT	GCCCTTCAACG	ACATTTGACGTGAGGCTCAGATTGATTTCTGTGTCAT	1178
Db	468	TGGAATTCACCT	TAATCTTTAAT	TGATTTGATTTGATGAGCTCAATTTGACTTTCTTCGCGGT	527
QY	1179	CAAGGATGGGG	CACACCGCGGAG	CGCCGCTCTGGGCACTTTTCAGAGAAACAAGCTTC	1238
Db	528	CAAGGATATG	GCATTTCTGA	ATACTGTCTCTGGGATCTTTCTTTCGCAATGAAATGCC	587
QY	1239	CTCTCCATCA	CAAGCAGTGG	CCACGTGCGCGGTCTGAGTTCCAGATCCAGATCCAC	1298
Db	588	TTCCAGATGG	CAGCAGTGGG	CAATATGTTGCTTGGAAATTTCAGTGTGACATTCAC	647
QY	1299	AGGGAAGGGG	CTTAAATCAT	CTTTTACCACTTTCCGACAAACGAGTCCCGGATCC	1358
Db	648	TACTGGCAG	AGGGTTCA	ATCATCTTACACCACTTTGTCAGATGAGTGCATGATCC	707
QY	1359	TGGCGCTTC	AGTAATTTGG	CAAAACGGTTTGAGGGAACAGCTCCAGCTGGGCACTCATCTC	1418
Db	708	TGGCTTCT	TATTAACG	ACACGCTTTTGTGTGACAGGTTTCTACTCGGGAAGCTGGTTTC	767
QY	1419	CTTCTCTGT	ATGAGGCTT	CTTGGGACTCAAGGACTCAGAGACCATCACTGCTGCT	1478
Db	768	TTTCACTGT	ATGATGACTT	TGTTCAGAACCAAGGATTCGAGTCAATTACTGTGATACT	827
QY	1479	GAAAGAGGG	CACCGTGTCTG	GAACAGGCTGTGTGGGTGTGAAGTCCCTGTGTGGT	1538
Db	828	GCAAGACGG	GAACGTTGT	GTGAAGTCCACCGTGTGTAAGTCTCATGTGTGGT	887
QY	1539	TCACCTGACTT	CGCCACG	GCACCATCTCTTCGCGGCTTGCCTGCTCTTCAAGGA	1598
Db	888	ACATCTGA	CAGGCTC	ACAGCGAGTCAATTTTGCTCTCTGGAATGGCCAGGATTTATTAAGA	947
QY	1599	TGCCTTGA	CTGTGTGGT	GTGAGGCCCCAGCGGCTAACCCCATCAAAATCACTT	1658
Db	948	TTCTTTAT	TATGTGATG	ATTAATTTGAAGCAAAACCAAGCCACTCTTCAAAATAACTTT	1007
QY	1659	CGACGATTT	CAAAACG	AGGTCAACTATNAGACACCCTGTGAATGAGCATTTGGCGGAGCTTA	1718
Db	1008	TGACGATTT	CAGACAG	GTCAATTAATNAGACACTTTGAGGTCAAGATGAGGACAGCCAG	1067
QY	1719	CTCAAGCGC	CTTGATCG	GGGTTTACACAGGGAACCCAGGTTCCCAAGTTCTCATCAGAC	1778
Db	1068	TTGCGCC	CACTGATCG	CGAGTACACGGAACCCAGGATCCCAAGTTCTCATCAGAC	1127
QY	1779	CAGCAACT	ACTTACTTCT	CTTCTTACCGGACAAAGTCACTTGGACATCGGCTTCA	1838
Db	1128	CGGGAATTC	ATGATGCT	CTTATTCACATGACAAACGCGCTTCAGACATCGGCTTCT	1187
QY	1839	GCTCCGCT	ATAGACT	ATATAACATGCACTCAGACCATCTGTGATCCAGGAATCCAGT	1898
Db	1188	CATCACT	ATAGAGTGA	CGCTTGATCGGATTTCTGTGCTTGACCCGGGCAATCCGT	1247
QY	1899	AAATGAC	AGCGTCAT	TGGAAATGACTTTACGTGGCGCGCTGTGACTTTCAGCTGTGA	1958
Db	1248	GAA	CGCCAT	ATGCGCCAGGTGGAGCTTTTGGATCAGGTTCACAGTGACTTTTCACTGTGA	1307

QY	1959	CTCGGGGCTACACATTAATATGACGGGGAGCCTCTGGAGTGTAGAGCCAACTTCCAGTGGAG	2018
4Db	1308	CCCGGGGATACACTTAAGTGAACAGACCCCTGTCTGTAGAGAAACACCAAGTGGAA	1367
QY	2019	CCGGGCGCTGGCCACAGTTGTGAAAGCTCTCTGTGTGGCTTCAATTAAAGGCTTCAGTGGGAC	2078
Db	1368	CCAGCCCTTGGCCAGCTCGAAGCTCTATGTGTAGAGGCTACACTCAAGGAAAGATGGAAAC	1427
QY	2079	CATCTTGTGGCCAGGGTTCCCTGACTTACCCCAACATTGAACTGGACCTTGATAT	2138
Db	1428	AGTCTCTTCTCTCGTGGGTTTCCAGATTTTATTCGAAACCTCTTAAACATGACGTGGACAT	1487
QY	2139	CGAAACATCTCATGGCCAGGGTGTCTTCACTTTCACACCTTTCACCTCGAAGAAATGG	2198
Db	1488	TGAATGTCTCATGGGAAAGGATTCAAATATCTTTCACACCTTTCATCTTGAAGTTC	1547
QY	2199	CCATGACTACCTCCCTCATCTAGTGAAGCGGACGCTTCCACCGAGCCCTGAGGCGCTAAC	2258
Db	1548	CCACGACTATTTACTGATTCACAGAGGATGGAAGTTTTTCCGAGCCCGTTGCCAGGCTCAC	1607
QY	2259	TGGATCTGGGCTGGCCAGCTCCCATCAGCGTGGGCTCTATGGCACTTCACTGGCCAGT	2318
Db	1608	GGGGTGGGTGGTGGCTCATACGATCAAGGACGGCCTGTTGGAAACTTCACTGCCACGCT	1667
QY	2319	CCGCTTCACTCTGTATTTCTGCATGTATATGAAAGATTCAACATCACTTCTCAGAGTA	2378
Db	1668	TGGGTTTATATCAGACTTCTCAATTTCTTAAGAGGGCTTCAATATCATTTCAGATA	1727
QY	2379	CGACTTGGAGCCCTGTGAGGAGCCGAGAGTCCAGCCATCAGCATCCGGAAAGGGCTTGA	2438
Db	1728	TGACTTGGAGCCATGTGATGATCTCTGAGTCCCTGCTTCCAGCCGAAAGAAATTTGGTTTCA	1787
QY	2439	GTTTGGCGTGGGCGCACACTTTCCTCTCTGCTTCCCGGGTATCCGTCTGAGAGGCGAC	2498
Db	1788	CTTTGGTGTGGGAGACTCTGTGAGTTTCTGCTCTCGGAGATATGTTTGAAGGTGC	1847
QY	2499	CGCCCGCATCACGTGCTCTGGGGGGCGACGCGCCTGTGAGCTCGCTCTGCCAAGTGT	2558
Db	1848	CTCCAAAGCTTACCTGCTCTGGGGGGCGCGCTGTGTGAGTCACTCTGCGCAAGGTG	1907
QY	2559	TGTTGCTAGTGTGGGAATTCAGTACACAGGAGCTCAAGGATCTTGTGCTGCCCACTT	2618
Db	1908	TGTGGCCGAATGTGGAGCAAGTGTCAAAAGGAAATGAAGAACTTACTGTCTCAAAATTT	1967
QY	2619	TCTCTGTGAATACATTAACAATTCATGATGATCTACTCTCATCCAGACCCAGCCAGGGAA	2678
Db	1968	TCCATCCAAATTAATGATTAATTAACATGATGTATCTATAAATTAABAACAGAGCGGCAA	2027
QY	2679	GGGAATTCAGCTGAAGCCAGGGCATTCGAATCTCCGAGAGAGATGCTCTCAAGTTTA	2738
Db	2028	GGGCACTCACCTTAGAACACAGAACCTTCCACTTTTGAAGGAGATCTCTTAAAGGTATA	2087
QY	2739	TGATGGCAACAACAATCTCGCCCGCTGTCTGTGGAGTTTTTAGCATTCGTAGATGATGGG	2798
Db	2088	TGATGAAAAGACAGTTCTTCAACGTCCACTGGGACGTTCACTTAAATATGAATCTTGGG	2147
QY	2799	GGTGACTTTGAAACAGACATCCAGAGTCTGTGCTTGATTTCACTGATGCTGTAATA	2858
Db	2148	GCTGATCTCTTAAACAGACATCCATCACTTGTGCTAGATTTCAACACCAATGGAATCTGA	2207
QY	2859	CACGAGCAGGGCTTTGAAGTGCATTTTCCAGCTTTGAAGTCAATCAATGTGAGAACCC	2918
Db	2208	CACGACCAAGGTTTCAACTCACTATACAGATTTGATCTGGTAAATGTGAGATTC	2267
QY	2919	AGGAACCCCCAAGTTTGGCTACAAAGTTCAATGATGAAGAGTCAATTTTGCAGAGAGCTCCGT	2978
Db	2268	GGGCACTCCCTACTACGCGCTATAGAGATCCGATGAAGGCGCACTTTCACGACATGTAGT	2327
QY	2979	GTCCTTACAGCTGTGACCTCTGATATCAGGCTCTCGGGGTAGTGAAGAGCTGCTGTCTGAG	3038
Db	2328	TCTGTACAGTTTGCACACCCGGGGTACGCAATGCAATGCGACGACACCTGTACCTGTTTGGAG	2387
QY	3039	TGGAAGCGCCGAGCTTGGGACCGGCGCTTGGCCACCTGTGTGCGCGAGATGTGAGGAGAC	3098

Db	2388	TGGAGACAGAGAGTGTGGGCAAAACCACTACCTTCTGTACATAGCGGAATGTGTGTCTCA	2447
Oy	3099	AGTAGAGAGAGAGGTGTGTGGGGCAGGTGTGTCTGTACACCCGGGATATCAAGTCCCTATGAAACA	3158
Db	2448	GATCCATGACAGCCACATCAGGAGCAATATGTGTCTCCCTGGGTATCAGCTCCGTATGACAA	2507
Oy	3159	CAATCTCACTGTCACTGTGACCAATCTGAAGCAGAGGGCCGGCTGTGCACCAATTTGGGCTACACTT	3218
Db	2508	CAACCTCCACCTGTCACTGTGATTAATGAGGGCAGACCCAGGAAAGACCAATATGAGCTCTCCACTTT	2567
Oy	3219	CCGTGTGTTTACACAGAGAGGTTTCAAGACGTCTGTCCGCACTTGGGATGGGCTGTGGA	3278
Db	2568	CATGTGTTTTCGACACAGGAGATGGCTCAAGCATCTCTCAAGGTCTGGGACGGGCGGTGGA	2627
Oy	3279	GAGCGGGGTTCTGCTGAAAGAGCTGAGTGGCCCGGCTCTGTCCAAAGACCTGTCAATAGAC	3338
Db	2628	CAGTGACATCTCGCTGTGAAGAGTGGAGTGGCTCTCGCCCTTCCGAGAGACATCCACAGACAC	2687
Oy	3339	CTTCAACCTCGGTGTGCTCGGATTCAGACACTGATTTCTTTCACAGCAAGAGGGCTTTTGC	3398
Db	2688	CTTCAACTCACTACACCTGTGCACTTTCGACAGGACCTTTCTTCAATCAGCAATGTGTGCTTCTC	2747
Oy	3399	CATTCAATTTTCAAGTGTCAACAGCAACGTCTCTGCAATGACCTTGGATATCCGCAAAATGG	3458
Db	2748	CATCCAGATTTCCACCTCAATTTGACAGCCACTGTAAACGATCAAGTATGCCCCAAATATGG	2807
Oy	3459	GAGTCGAGTGTGTACAGTTTGGGAAAGCCGGGACCTCCACAGTGTTCAGTGTGACCCCTGG	3518
Db	2808	CACCCGCTATGAGACAGACAGAGAGGCTGTGAGACACGCTCAATTTCCAGTGTGACCTCTGG	2867
Oy	3519	CTACGCGCTGAGGGAAGTGCAGAGATCAGCTGTGTGAAAGATTCAGAAACAGGTTCTTCTG	3578
Db	2868	CTATCAGTCTCAAGGACAAAGCAAAATACCTGTGTGTGACGTGAATAACCGGTTCTTTTG	2927
Oy	3579	GCAGCCCAAGCCCGCCCAATATGATATGTCTCTCTGGGGGGGAACTTGCACAGACCAATCTGG	3638
Db	2928	GCAACCAAGACCTCTTACATGCATAGCTGTGTGTGAAAGGAATGTGACGGGCTCCAGACAGG	2987
Oy	3639	AGTACTCTCTCACCAAAATTAACCGAAGACCTTACCCGCAAGGAGAGTGTGACTGGAA	3698
Db	2988	TGTTATTTTGTACCCCACTACACAGCCGATATCTCTGGGAAGGAATGTGACTGGAG	3047
Oy	3699	AGTGACGCTTCAACGACTACGTATGTGCTCTGTGATTTAACTTTTAACTCTTGAGCC	3758
Db	3048	AGTAAAGATGAACCCGGGACTTTGTTCATGCGCTTGATTTCAAAAGTTTCAACATGAGACC	3107
Oy	3759	TGGCATATACATTCCTCCATATATTAAGACGAGACGGGACTCTCAAGCCCTCATATAGGAAG	3818
Db	3108	CAGCTATACCTTCTACACACTATATGAAAGGGGAAGATTTCAACAGCCCTCTCATTTGGAG	3167
Oy	3819	CTTCTATAGCTCCAGCTCCAGGCGGATTTGAAGACGACCAACGCTCTTCTCTGC	3878
Db	3168	TTACACAGGGCTCTCAGGCCCCAGAAAGATTAAGAGTGCAGGAAACGCTGTTTCTGGC	3227
Oy	3879	CTTCCGACGCAATGATCTGTGAGCAATGCTGGCTTCTGTCTATTAAGTAATAGAAAACCC	3938
Db	3228	ATTGTGGAGTATGTGCTCTCGTGGGCTTTCAAGGTTTCCCATATGAATTAAGAGAAACC	3287
Oy	3939	GCGGAGATCATGTTTGTGATTCCTGTGTTCCATCAAGAACCGCAACGGGTGGGGTCTGACCT	3998
Db	3288	ACGGGAAGCTTGTTTGTGAACCCAGGAATATATATGAATGGGACAAGATTTGGAACAGACTT	3347
Oy	3999	GAACTGGGCTCTCTCCGTCACTTACTGACGAGGGGCTTACGAATTTGAGGGGCACTC	4058
Db	3348	CAAGCTTTGGCTTCCACATCACTTCAACAGTGTGACTCTGGCTATTAAGATTTCTTGACCCCTC	3407
Oy	4059	GACCCGAGCTGATCTCGGGGCTGATGTGGGAAGCCGCTGTGGAACAATATCCCGGACAGT	4118
Db	3408	ATTCATCACTGTGTGATTTGGGGCTGATGGGAACCTTCTGTGGACCAAGTGTGCTCTC	3467
Oy	4119	CTGCACAGCCCTCTGTGGGGGACAGTATGTGGGTTTGGACGAGTGTGTTGTCTTCTCCCA	4178

Db	3468	CTGAAATGCTCCCTGTGGAGGCCAGTACAGGGATCAGAAAGGGTAGTTTATCACCAAA	3527
OY	4179	CTACCCCCAGAACTACACCACTGGACAGATCTGTTGTATTTTGTACTGTGCCCAAGA	4238
Db	3528	CTACCCCCATAATTACACACTGTGTCAAAATATGCTTATTTCATTCACGGTACCAAAAGGA	3587
OY	4239	CTATGTGGTGTGTTGGCAGATTGCGCTTCTTTCACACAGGCCCTCAACACAGTGATGAGGT	4298
Db	3588	ATTGTGTGTCTTTTGACAGATTTTGCTTATTTTCAGACAGCCCTGAATATTTTGGCAGATT	3647
OY	4299	TCACGACGGCCACAGCCAGCATCTCGCGGCTCTCAGCTCCCTCTCGGGCTTCCATACAGG	4358
Db	3648	ATTGTATGGAACCCATGACACAGGCCACATCTTCAGCTCACTTCGCGGGCTTCCTCAGG	3707
OY	4359	AGAAATCATGCGCCCTGGGCAACCTCCAAATCAAGTTCTCATTAAGTTCAAGCCCAAGGCTT	4418
Db	3708	GGAAACATTGCCCCCTTGGCTAGCTCAAAATTCAAATTTCTGCTCCGATTCAATGCAAGACGG	3767
OY	4419	CGCACACAGCCAGAGGCTTCCACTTTTGTCTACCAAGCGGTTCTTCGAACCAAGCCACGCA	4478
Db	3768	TGCCTCTGCGCCGGGCTTCCACTTTCGTATCAAGCTGTTTCTGTATCCAGTGCACCCCA	3827
OY	4479	GTCGACGCTCTGTGGCCGAACCCCGCTATGCGAANAAGGCTGGGAGTAACTTCTGAGTGGG	4538
Db	3828	ATGACGCTGTGTCCCGAGCCCAATACGGAAGAGAAATGTGTTCTGAGTTTCTGCCGG	3887
OY	4539	GGACATCGTCCGCTTTCGAATGCAATCTCCGCTATGCCCTGCAGGGGTTGCACAGATCGA	4598
Db	3888	CTCATGTGTCCGATTTGAGTTCACACCCGGGATACCTGCTTCAAGGTTTCAAGCGGCTTCA	3947
OY	4599	GTCGCTCCCTGTGCTGTGGGCGCTTGGGCCAATGGAATGTCTCAGCGCCACAGTGTGGT	4658
Db	3948	CTGCGACATCGGTGCCCAACCGCTTTGGACAGATGGAACGACAGATCCCACTGTGTGGT	4007
OY	4659	GCCGTTGTGAAGCAACTCACAGAGCGCAGGGGACCATCTGTATCCCTGCGCTTCCAGA	4718
Db	4008	AACCTGCAGTGGCAATTTTCACTCAACGAAGAGTACAACTGTATCCCGGCTACCTCGA	4067
OY	4719	GCCGTACTCAACAGCTCAACTGTGTGTGGAAGATGTGTGTCCTCCGAGGCGCTGGCAT	4778
Db	4068	GCCATATCGGAACAACTTGAACTGTATATGMAATCATATGTTACGGAGGCTCGGGAT	4127
OY	4779	CCAGATCCAACTGTGCAAGTTTGTGACACAGACAGAACTGGGACATCGCTGAAGATTTGA	4838
Db	4128	TCAGATCCAAATGATCAAGTTTGTGCCACGAGACAGAACTGGGATCTCCTTGAGATCCAGCA	4187
OY	4839	TGTTGCAGATTAACACTGTATACCATGTGGGAGTTTCTCAGAAACAAACGTGCTGCCCT	4898
Db	4188	TGTTGGGATGTGACCGCACCCACACTGGGAAGTTCCTCAAGGCACACAGTATCCGGCACT	4247
OY	4899	TCTGAACGCACTCCCAACGACCTCTACCTCATTTTCTACCTCAGATATCAGGATATCGC	4955
Db	4248	GCTGAACGTACTTCCAAACCACTCTACCTCATTTCAGTGTGACATTAATGTGTGGACAC	4307
OY	4959	AGCTGGCTTCACTTGAAGTACAAACCGTGGGCTGACAGTGTTCGGAACCTGTGT	5018
Db	4308	TGCTGTGTTTCCACTCGGAATACAAACCTGTAGTCTTGCTGCAATGCCAAACACGACCT	4367
OY	5019	GCCCACTAACGGGGTGAAGACTGGCGAGCGCTACTTGGTGAATATATGTGTGTCTTTTCCA	5078
Db	4368	CCCCACGAAACAGCATCAAAATCGGAGATCGGTACATGTGTGAACACAGTGTCTCTTCCA	4427
OY	5079	GTTGTAGCGGGATATGTGCTCTCAGGGGCAAGCCCACTATCTCTGCATGCCCGGAACAGT	5138
Db	4428	GTCGAGCCCGGGTACACCTCTGACAGGGCGGTTCACACTTTCCTGTATGCCAGGGACGT	4487
OY	5139	GCGGCGATGAACATACTCCTCTCCACTCTGTATTGCACAGTGTGGGGAAACAGTGGAGAA	5198
Db	4488	TGCGCGTTGGAACATACTCCGTCTCCCTGTGATTGCACCTGTGAGGGAGACGCTGAGAC	4547
OY	5199	CATGAGAGGGGATATCTGAGCGCCCGGTTCCAGGCAATACCCCAATTAATCATGGACMG	5258
Db	4548	CTTGGGTGTGTGATCTGAGCCCCGGCTTCCAGAGTTCTTAACCCCAACATTAGACTG	4607

5259 CTCCTGGAAAATAGCATGCGCGGTGGGCTTTGGAGCTCAATCCAGTCTGAACTTTC 5318
4608 CACTTGAGAGATCTTACCTTACCATCGGCTATGGTGACATATTCAGTTCTGAAATTTTC 4667
5319 CACCGAGCCCAACAGACTACATAGAAATCCGGAAATGGCCCTATAGACACCGCAT 5378
4668 TACCGAAGCTAATCATGACTTCTTGAATTCAGAAATGAGACTTACCAACACGAGCCAT 4727
5379 GATGGAAAGTTATGAGGAAGCAGCTTCCAGCTCCCTCTCTCCAGCTCCACGAGAC 5438
4728 GATTGACAAATTTAGGGGACGAGATCTCCCGCGGCTGCTGAGCAACGCGATMAAC 4787
5439 CACCGGTATTTCCAGAGGACACTCCAGAAATGGGCCAGATTCAGAGTGAAGTATCA 5498
4788 CCTCATTCACCTTTATATGTAACATTCGCAAAACCGGCAAGATTTAAATCTTCAACA 4847
5499 GGCCTATGAACCTTCAAGAGTGCCAGACCCAGAGCCCTTTCAGATGGCATTTGAGGGG 5558
4848 AGCTTATGAATTAACAGACTGTCCAGATCCACCCCATTTAGAAATGGGTACATGATCA 4907
5559 AGCTGCTTCAACAGTGGAGCAATCATGATCTTGAAGTCCCTCCGGGTATCAATTGAC 5618
4908 CTCGATTTACAGCTGGGGCAATCAGTATCTTTGAGGTATCTGGGTACATTTCAAT 4967
5619 TGGCCACCTGCTCAGCTGCAAGTCAATGGCAACCAACCGGAACTGGGACACCCCGTGC 5678
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RESULT 15
 AAD33318 standard; cDNA; 10673 BP.
 ID AAD33318;
 AC AAD33318;
 XX
 DT 01-JUL-2002 (first entry)
 DE Human C3b/C4b complement receptor like cDNA #1.
 XX
 XX Human; C3b/C4b complement receptor-like molecule; immune system disorder;
 KM gene therapy; rheumatoid arthritis; psoriatic arthritis; osteoarthritis;
 KM inflammatory arthritis; inflammatory joint disease; Alzheimer's disease;
 KM multiple sclerosis; inflammatory bowel disease; nervous system disorder;
 KM transplant rejection; autoimmune disease; ischaemic condition; nocturnal;
 KM metabolic disorder; immunomodulatory; neuroprotective; diabetes; lupus;
 KM infertility; vasodilator; obesity; cardiac; gene; ss.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH 334..9543
 FT CDS
 FT /product= "Human C3b/C4b complement receptor like protein
 FT #1"
 FT /transl_except= (pos:2416..2418, aa:Xaa)
 FT /note= "This translational exception occurs while
 FT decoding the alternative version of human C3b/C4b
 FT complement receptor like protein #1 (AAE20900)."
 XX
 XX MO200210199-A2.
 XX
 XX PD 07-FEB-2002.
 XX
 XX PF 24-JUL-2001; 2001MO-US023232.
 XX
 XX PR 02-APR-2000; 2000US-0222504P.
 XX
 XX PR 28-NOV-2000; 2000US-00728787.
 XX
 XX PA (AMGB-) AMGEN INC.
 XX
 XX PI Welcher AA, Elliott GS;
 XX
 XX DR WPI; 2002-303934/34.
 XX
 XX DR P-PSDB; AAE20787, AAE20900.
 XX
 XX PT Nucleic acid encoding a novel C3b/C4b Complement Receptor-like nucleic

PT acid molecule, useful for treating, preventing and diagnosing rheumatoid
 PT arthritis, psoriatic arthritis, inflammatory arthritis, and multiple
 PT sclerosis.
 XX
 XX Claim 1; Fig 1; 251pp; English.
 XX
 XX The invention relates to a nucleic acid encoding a novel C3b/C4b
 CC complement receptor (CR)-like nucleic acid molecule. The C3b/C4b CR-like
 CC polypeptide and nucleic acid molecules may be used to treat, prevent,
 CC ameliorate, diagnose and/or detect diseases such as immune system
 CC disorders such as rheumatoid arthritis, psoriatic arthritis, inflammatory
 CC arthritis, osteoarthritis, inflammatory joint disease, autoimmune
 CC disease, multiple sclerosis, lupus, inflammatory bowel disease,
 CC transplant rejection, nervous system disorders (e.g. Alzheimer's
 CC disease), ischemic conditions, metabolic disorders (e.g. obesity and
 CC diabetes) and infertility. The invention is useful in gene therapy. The
 CC present sequence is human C3b/C4b complement receptor like cDNA
 XX
 SQ Sequence 10673 BP; 2690 A; 2711 C; 2574 G; 2691 T; 0 U; 7 Other;
 Query Match 40.1%; Score 4067.4; DB 6; Length 10673;
 Best Local Similarity 65.5%; Pred. No. 0;
 Matches 6001; Conservative 5; Mismatches 3136; Indels 25; Gaps 3;
 QY 819 AGAGATCGAGCAGGCGAGTTGGCGGTGACCTGGCATACCTGCATATGCGCGAGGAGG 878
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 QY 939 GGGACGAAGGCAATATATCCCAAAAGAAATACATATGTCGGCTTAAGAGCAGCTG 998
 DB 528 GGGGGAAGATATATCACTGTGACGAAACATATGATGTCGGCAAGGCCAGCTG 587
 QY 999 CGGTCTCTCTCTCTTCACTTCAACAGCCGCTGCGGAGTGTCTGTCTCCCACTA 1058
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Db	2222	GCGACTTTTCAAAATGAGGCTCTTGTGTCTCAATTTTCAGCGACTTTCAGCTCAAGAAAT	2281
OY	6032	GCCCTCCTCCCAACCATCTCCCTCCCAACGCGGAAGTGTGCACAGAGATGAAATTCATA	6091
Db	2282	GTCAAACCTCCCGACGCGGTTCACAGCGAGAAATGCTTACTGAGGATATGATTTCCAGA	2341
OY	6092	TAGGTGACATGTACGCTACAGATGCTTCCTGCTTACTTATGTGGGGAATGAATTC	6151
Db	2342	TAGGAGATTTTGTGAAGTACAGATGCTCACCCGCGGTACACTTGGTGGGACCACTTC	2401
OY	6152	TGACCTGAAACTTGGAACTTACCTGCAGTTTGAAGACCAOCCCGGATATGTAAAGTC	6211
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OY	6212	ACTGTCCAACAAATAGCTTTCGACAGACTCCAACAGCGGTATCTCGACCGACAGTACC	6271
Db	2462	AATGCCACGCAATATGAAGTCCGAGCTGATCATCGGAGTCAATTCTCAGTCCAGGATAC	2521
OY	6272	CTGGAACTATCCCGAGTTCCAGACTGCTCTTGGCTGTGAAGATGAGCCCGACTATA	6331
Db	2522	CGGGATATTTATTTAACTCCGAGACTTCTCTTGGAGATTTAAAGTGGAAACCAACTACA	2581
OY	6332	ACATCTCCCTCAGAGTGGATATCTCTCAGCGAGAAACAAATATATGATTTGAGATTT	6391
Db	2582	ACATTACCATCTTGTGTGACACATTTCAAAGTGAAMACATGTGTGATCAGCTGAAGGT	2641
OY	6392	TTGATGTGTCATCAGAGCAGAGTCTCTGCTGTAAGGCCCTGAGTGGGAATTACTCAGCTC	6451
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OY	6512	ACATTCGGAAGGGCTTCAAGATCCGCTATTACAGCCCTTACTGCAAGCTGCCAGGCTC	6571
Db	2762	CCAGTAAAGAAAGATTCAAGATTCCTCTATGACGACCTTTACTGCAAGTTGACCAACCCC	2821
OY	6572	CACCTCATAGGCTTCACTCTAGGCCAGACCAAGAACCCGCGGGGCTCCATCCACTTGG	6631
Db	2822	TGAGAAATGGGGGATATTCTTAAACAGACTGCGAGAGCGGTGGAAAGCAAGTGCATTAAT	2881
OY	6632	GCTGCAAGCGCGCTTACCGCGCTGTGTGGGACACAGCATGGCCATCTGTATCCCGGACCCC	6691
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OY	6692	AAGGCTACCACTGTGAGCGAAGCCATCTCTCTGCAGACTTCTTCTGTGGGCTTC	6751
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OY	6752	CTGAGGCCCCCAAGAAATGGAATGTGTGTGGCAAGGAATTAACAAGTGGGAACCAAGCCG	6811
Db	3002	CAGAAATCCCCAGGAAACGTTCTATTACCGGGAGAAATTAACCTTTGACAGTAAAGTG	3061
OY	6812	TGTACAGCTGCAGTGAAGGCTACCACTCCAGGCAAGCGCTGAAGGCCACTGCAGAGTTC	6871
Db	3062	TCTAAGATGTCAATGAGGGCTTCAAGCTTGAATTCAGCCAGACAAACAGCCGTGTCT	3121
OY	6872	TGACACAGGCGCTATGAGCAACGCGCAATGTCCACCAAGTGTGCCCTGTGACTTGTCT	6931
Db	3122	AAGAAGATGGGCTGTGAGTAAACAAGGGGAAGCGCCCATGTGTAAAGCCGGTCCGCTGCC	3181
OY	6932	CTGATGTCAATGAGCATCAGCGTGGAGCATGGCCCATGAGGCTTAATCTTTAGACACAGT	6991
Db	3182	CCAGCATTGAAGCTCAGCTCTTCAGAACATGTCAATCTGAGGCTGTGTTCAAGATCTTTGA	3241
OY	6992	ATCAGTTTCCAGGCGCAGCTGATGTCACTCTGTGCAACCTGTGGCTACTACTATCTGGCCAA	7051
Db	3242	ATGATATGCGTCTCAAGATTTGTCTGAGAGCTGCAAGTCTGTGTATCTAATTAAGAGGCTGA	3301
OY	7052	GAGTATCCGCTGTGAGGCGCAATGGCAATGAGAGCTCGGGGACTTAAGCCCACTGACC	7111

Dp	3302	GGCTTCCTGGGTTGCCAGGCCCAATGGGACGTGGACATATAGAGATGAGAGGCCAAGCTGTC	3361
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Dp	3362	GA-----	3363
Qy	7172	CTGTCTACGGGGCAACAGCCATCTTCTCTCGCAATTCGGATATACACTGTTGGGCTCCA	7231
Dp	3364	-----	3363
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Dp	3364	-----GCTG 3367	
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Qy	7352	ACCGGGGACGTGTGTGTACCAATGCAATGCTGGCTTCGGCTGATGGCAATGCTCTGC	7411
Dp	3428	ACAGAGACACCGTGGTTTACAGAGCAATCTGTGTTCCGGCTTGTGGGAATTCCTCGTGA	3487
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Dp	3488	GGATATGCTCTCAAGACCAACAGATGTGTGACAAAGCCCTGTCTGTGTCCCATACAT	3547
Qy	7472	GTGGACACCCAGGCAACCTGTGTCACAGCCCTCACTCAGGGTAAACAGTTTAACTCAAG	7531
Dp	3548	GTGTGCACCCCTGGAACCCCTGCCACGGATTCACTAATGGCAGATGTCAACCTGAATG	3607
Qy	7532	ATGTGTCAAGTTTGTGTCACACCTGGGATATATGCTGAGGGGGCTGCTAAGTCCAAAT	7591
Dp	3608	ATGTCTGTAATTTCACTCGCAACACCGGGCTATTTGTCTGCAAGGGGCTGTCTCGAACCCAGT	3667
Qy	7592	GCTTGGCCAGGGGGCAATGAGTGACATAGCTGCCACCTGCAAGATCATCAACTGTACAG	7651
Dp	3668	GTCCGAGCAACGGCCAGTGGAGTACCTCTGCCCCAGTGTGAGTGTGAACGTGTCTG	3727
Qy	7652	ATCTGCACACCAAGAAATATGTTGCTGTCAGTGTCCACGACGGGCCCGCACAGTTTCA	7711
Dp	3728	ATCCAGGCTTTGTGTGAAAAATGCCATTGTCACGGGCAACAGAACTTCCCTGAGAGTTTG	3787
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Dp	3788	AGTATGGAATGATATCTCTGATTCATGCAAGAGGATTTTACTGTCTGGATCTTCAG	3847
Qy	7772	TGCTCAGCTGCACAGGAGATGGCACATGGGACCGTCCCCCGCCAGTGTCTCTTGGTGT	7831
Dp	3848	CCTTGACCTGTATGGAACAAATGGCTTAATGGGACCGATCCCTGCCCAAGTGTGTGCTATAT	3907
Qy	7832	CCGTGAGCCATCCGGGGGCTCCCGGCTCACTCCAGATGTCTTGAGACAGTTATCTGTGG	7891
Dp	3908	CTGTGACACCCACAGGGGTCCCTGTCACACGCCGCTCTCATCTGGAGAGCTGTTTACATATG	3967
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Dp	3968	GCGCGGTGTGCATCACTCCTGACGAGGAGCGAGAGCGTCAATGAGCAACGACGAGAG	4027
Qy	7952	TGTGTGGGCTGGATGAGACCTGGAATGGCTTCCTTCCTCACTGCTCAGAAACAGCGTGG	8011
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Qy	8012	GAGTTTGGGAGACCCCTGGGATTCGCCGCTCATGGCAATCCGTTTGGGGGACAGCTTGATCT	8071
Dp	4088	GATTTCTGTGGTATCCGGGGACCCCAAGCACATGGGCTCTCGGCTTGTGTATGACTTTTAA	4147
Qy	8072	CAGGCACTGTATGCGCTTCACTGTGTGAGCTGGCCACGTGCTCCGGGATTCGTCAAGAC	8131
Dp	4148	CAAGAGCTTCTCTCGGCTTCTCTGTGAATATGGGGACACAGCTAAGGGGGCTCCCTGAAAC	4207
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 Db 4388 ATTGCACAGCCAAAGGAGACCTGAGCAGGACCTGCTCCGACTGCAACAATATTAAGTGTG 4447
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RESULT 2
 AY407075
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 DEFINITION
 Mus musculus CSMD1 gene, VIRUAL TRANSCRIPT, partial sequence.
 ACCESSION
 AY407075
 VERSION
 AY407075.1 GI:39763046
 KEYWORDS
 GSS.
 SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE
 AUTHORS
 Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
 Todd, M.A., Tarenbaum, D.M., Civello, D.B., Lu, F., Murphy, B.,
 Perriere, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
 Adams, M.D. and Cargill, M.
 Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios
 JOURNAL
 Science 302 (5652), 1960-1963 (2003)
 PUBMED
 14671302
 REFERENCE
 2 (bases 1 to 5901)
 AUTHORS
 Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,

Todd, M.A., Tanenbaum, D.M., Civeille, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
Adams, M.D. and Cargill, M.

TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.

FEATURES Location/Qualifiers

source

1..5901

/organism="Mus musculus"

/mol_type="genomic DNA"

/db_xref="taxon:10090"

gene

<1..>5901

/gene="CSMD1"

/locus_tag="HMC2769"

ORIGIN

Query Match 19.8%; Score 2011.6; DB 9; Length 5901;

Best Local Similarity 58.0%; Pred. No. 0;

Matches 3609; Conservative 0; Mismatches 2290; Indels 328; Gaps 7;

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OY 3752 TGGAGCTTGCTATGATCTTCTCATATCTACGACGAGGAGCTCTTCAGCCCTCTCA 3811
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DB 2 TGGAGCCGAGTTATGATCTTCTCATATCTATGAGGAGGAGAGCTCCACAGCCCACTGA 61
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OY 3812 TAGGAGCTTCTATGCTGCCAGCTCCAGGCGGCATTTGAAACAGACAGAAAGCTCT 3871
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DB 62 TTGGAAGTTCCAGGGCTCTCAAGCCCAAGAGAGATCGAGACAGTGTAAACAGCTCT 121
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OY 3872 TCTCCGCTCCGACAGATGATCTGTGACATGCTGCTGCTCATATGACATATACAG 3931
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DB 122 TTCTGGCATTCAGAGATGATCTTCTGTGCTGTGCGGATTCGCGATTTAAATTTAA 181
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OY 3932 AAAACCCGCGAGATCATGTTTGTATCTGCTTCATCAAGAACGCGACACGCGTGGGT 3991
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OY 3992 CCGACTGAAGCTGGGTCTCTCCGTCACTCACTACCTGCGGCGCTACGAAGTTGAG 4051
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OY 4052 GCACCTGCACCTGAGCTGATCTGTGGGCGCTGATGAGGAAGCCGTGTGAAACATCCC 4111
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DB 302 ATCCCTGCTCATTTGATGATGTGTACAGAGGCTGATGGAAGCCGTCTG----- 350
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OY 4112 GGCAGATCTGCACAGCCCTGTGTGGGAGACAGTATGTGGTTGCGACGAGTGTCTTGT 4171
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DB 351 -----GCAACCTGTGTGAGGCGCAATACCGGCTCGAGGGGGTGTGTTGT 396
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OY 4172 CCCCCAATGCCCCAGAACTACACCAAGTGAAGATCTGCTGTATTTTGTACTGTGC 4231
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DB 397 CACCAAACTACCTCTATTAATACACAGCTGGGCAAGTGTGATCTATTCATACAGGTG 456
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OY 4232 CCAAGGACTATGTGATTTGGCAGTTGCGCTTCTTTCAACAGGCGCTCAAGAGTGG 4291
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DB 457 CCAAGGAATTCGATGATTTGAAAGATTTGCAATTTCCAGCTGACATGAAGACTGG 516
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OY 4292 TGGAGTTCAAGACGCGACAGCCAGCACTCGCGGCTCTCAGCTCCTCTCGGGCTCCC 4351
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DB 517 CAGAGTTGTTTGTATGGAACATCTCCAGGCGAGGCT----- 553
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OY 4352 ATACAGAGAAATACATGCTCTTGGCCATCTCCATCAATGCTTCAATTAAGTTACAGGCCA 4411
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DB 554 -----TGTAACAATCTGCACTGCTACATCAATCAATGATTTGCTTGAATTCAGCGCCA 608
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OY 4412 AAGGCTCGACAGCAGAGGCTTCACTTTGTCTACCAAGGAGTTCCTCGAACAGCG 4471
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DB 609 AAAGCGAGCTTTGTCACGGGGTTTCCACTTCGTTACCAAGCTGTTCCGCGACCAAGTG 668
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OY 4472 CCAAGGAGTCACTGTGTCGCGAACCCCGCTATGCAAGAGCTGGGAGTGAATCTTCT 4531
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DB 669 ATACAGATGCACTGTGCTCCGAGACCGAGATATGGGAAGAGATTGGTTCTGAGTTCT 728
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OY 4532 CGGTGGGGGCAATCGTCCGCTTGAATGCAATCCGGCTATGCTTGACAGGGTCCGACG 4591
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DB 729 CCGAGAGCTTCATCGTCCGCTTGAATGCAATCCGGCTATGCTTGACAGGGTCCGACG 788
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OY 4592 AGATCAGTGCCTCCCTGTGCTGGGAGCTTGGCCCAATGGAATGTTCTAGCGCCACGT 4651
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DB 789 CCATCCGCTGCCAGTGTGTGCCAAATGCTTTGGCTCAGTGAATGACATCATCCAAAGCT 848
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OY 4652 GTGTGTGCCGTGTGAGGCAACTCAGAGGCGAGGGGACCATCTCTGCTCCCTGGCT 4711
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DB 849 GTGTATTTCCATGCACTGCAATCTTCACTCAGAGGAAGAGAGATTTGTCTCCAGGCT 908
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OY 4712 TCCCAAGCGCTACCTCAACAGCTCACTGTGTGGAAGATCGTGTCTCCGAGGCG 4771
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DB 909 ATCTAGGCTCTATGGAACCACTAATCTGTGTGGAAGATCATATGATCGAGGGCT 968
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OY 4772 CTGGCATCCAGATCCAAAGTTGTCAATTTGTGACAGAGCAAACTGGGACTCGCTGAA 4831
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OY 4832 TATTGATGTGACATTAACATGTTAACATGCTGTGGGAGTTCTCAGAAACAAGCTGC 4891
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DB 1029 TCCATGATGAGAGACATGACGCGCCGAGACTGGGAGCTTCTCAGNNNNNNNNNN 1088
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OY 4892 CTGCCCTTGAAACAGACCTCAACAGCTCACTTCACTCAGATATCAGCG 4951
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OY 4952 TATCTGACAGCTGCTTCACTTGAGATACAAACGCTGGGCTGACAGTGTCTCGGAA 5011
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OY 5012 CTGCTGTGCCAGTAAACGAGGTGAAGCTGGGAGGCTAATTGTTGAATGATGTGTGT 5071
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OY 5072 CTTTCAGTGTAGCGGGGATATGCGCTCAAGGGCCAGCCCAATCTCTGATGACCGG 5131
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OY 5132 GAACAGTGGCGGATGAATCACTCCCTCTCACTCTGTATTTGACAGTGTGGGGAACAG 5191
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OY 5192 TGAAGGAGATGAAGGGGTGATCTGAGCCCGGCTTCCAGGCAATCAACCAATGAAC 5251
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DB 1389 TAAACAGATGAGTGAATGATCTGAGCCAGGGTTCACAGGCTCATACCCCAACATCT 1448
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OY 5252 TGAATGCTCTCCGGAATAATGACATGCGCGGCTTTGAGAGTCAATCCAGTTCTGA 5311
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DB 1449 TGAATGCTCTCCGGAATAATGACATGCGCGGCTTTGAGAGTCAATCCAGTTCTGA 1508
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OY 5312 ACTTCTCCACGAGCCCAACAGATACATAGAAATTCGGAATGAGCCCTATGAGACCA 5371
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DB 1509 ATTCTCAACTGAAGCAACATGATCTTACCTGAGATTCAGAAATGAGCCCTTACAGACA 1568
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OY 5372 GCCGATGATGGAAGATTCAGTGAAGGAGCTTCAAGCTCTCTCTCAAGTCCC 5431
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Db	3189	ATGAATAACGAACCTCAAGTTCCTCCACACTGACGCCCGCGCTACTTCTTGAAGGGTTCAGA	3248
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Qy	7472	GTGACACCCAGGCAACCTGTCTCAACGAGCTCACTCAAGGGTAAACAGTTAAACCTCAAG	7531
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RESULT 3
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Mus musculus 10 days neonate cerebellum cDNA, RIKEN full-length
domains 1, full insert sequence.
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ACCESSION
AK081081.1 GI:26099665
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
10349636
2
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20493374
11042159
3
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Kono, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matsubara, Y.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861
4
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
The RIKEN Genome Exploration Research Group Phase II Team and the
PANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
The PANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 3882)
7
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
Aochi, J., Aizawa, K., Akimura, T., Arawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Kato, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Nunazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
Direct Submission
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Kanagawa 230-0045, Japan (E-mail: genome-res@gs.c.riken.jp,
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)

COMMENT
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/
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Best Local Similarity 69.5%; Pred. No. 0;
Matches 2507; Conservative 0; Mismatches 1098; Indels 1; Gaps 1;
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1 TGGCATCCACCTGATATGGAAGCGAGCTGGAGACGCTTCTGATGAGACACGCTCAC 60
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 Pan troglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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 1 (bases 1 to 5824)
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
 Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
 Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sinsky,J.J.,
 Adams,M.D. and Cargill,M.
 Inferring nonneutral evolution from human-chimp-mouse orthologous

JOURNAL Science 302 (5652), 1960-1963 (2003)
 PUBMED 14671302
 REFERENCE 2 (bases 1 to 5824)
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
 Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
 Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sinsky,J.J.,
 Adams,M.D. and Cargill,M.
 TITLE Direct Submission
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
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 them based on alignment.
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QY 8398 CTTGGGCTGGCAATGATCTGATGATACAACTGTGATATCATGTGTGTCCGCGC 8457
DB 4268 NNN 4327
QY 8458 TATATGATGATGATCATAGATATCTGTGTGAGTGCACCAAGACCGGACATGAAAT 8517
DB 4328 NNN 4387
QY 8518 GGAACCAAGCCGCTCTGAAAGCTCTCATGTGCAAGCACTCGCTCATGCCAATGG 8577
DB 4388 NNN 4447
QY 8578 AAGGTGTGGGTGTGATCTCATGTGGGCTCAAGTGTGATGCTGCTGAGAGGG 8637
DB 4448 NNN 4507
QY 8638 TACAGCTCTCCGCGCGGCTTCACTGTGAGGAAATGGGTCTGAGCCGAGAG 8697
DB 4508 NNN 4567
QY 8698 CTGCTAGTGTCTCTGTGTCTGTGGGAGATCTGTGTCTCCGCTCCGTGAGAGAGA 8757
DB 4568 NNN 4627
QY 8758 GAGGACGAGGCTTCTCTACAGTCACTGTCTCTCTCTGCAATCCCTGTGTG 8817
DB 4628 NNN 4687
QY 8818 CTGTGGGCTCTCAAGCAAGTTTCCAGTCAATGAGCATGAGTGTGACACCAAGCCC 8877
DB 4688 NNN 4747
QY 8878 AGCTGATATATCGAACCTGCAACAGTGTGGGACCTGTGTGTGCAAGTTTGGATA 8937
DB 4748 NNN 4807
QY 8938 CAGAACATTTCTAGGCTTACAGGTTGGAAGCAGTCTCTTCTGTTGTCAAAAGG 8997
DB 4808 NNN 4867
QY 8998 TACTCTTGAGGCTTCAACACAGAGCTGCTCCAAAAGCTGACTGAGTGAAC 9057

[illegible]

VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
BA478219.1	GI:31912870	EST.	Homo sapiens (human)					
			Homo sapiens					
			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.					
			1 (bases 1 to 651)					
			Amorze,W., Krieger,S., Regiert,T., Rittmuller,C., Schwager,B., Mewes,H.W., Weill,B., Amlid,C., Osanger,A., Fobo,G., Han,M. and Wiemann,S.					
			EST (Amorze,W., Krieger,S., Regiert,T., Rittmuller,C., et al.)					
			Unpublished (2003)					
			Contact: MIPS					
			MIPS					
			Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany					
			This is the 5' sequence of the clone insert					
			Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; Heidelberg/Germany) within the CDNA sequencing consortium of the German Genome Project.					
			No sl sequence available.					
			This clone (DKFZ668606203) is available at the RZPD in Berlin.					
			Please clone the RZPD: Resourcenentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.					
			Location/Qualifiers					
			1..651					
			/organism="Homo sapiens"					
			/mol_type="mRNA"					
			/db_xref="taxon:9606"					
			/clone="DKFZ668606203"					
			/dev_stage="adult"					
			/lab_host="DH10B"					
			/clone_lib="686 (synonym: hlcc3)"					
			/note="Vector: pRiplex2; Site_1: SfiI; Site_2: SfiI; cDNA-collection"					
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			Query Match					
			Best Local Similarity 100.0%; Pred. No. 1.5e-144; Length 651;					
			Matches 635; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
			9253 AGGTCCGCGCCAGTGGAGAGACCATCAACATGCGCGGAGCCACCGCTCACCAAGCTT					
			17 AGTCCGCGCCAGTGGAGAGACCATCAACATGCGCGGAGCCACCGCTCACCAAGCTT					
			9313 TGATTTCTGTGGAGATGTTTTTGGCCAAAGATTCCTGTGTGGAAAGGGGCTTGAATACCAAG					
			77 TGATTTCTGTGGAGATGTTTTTGGCCAAAGATTCCTGTGTGGAAAGGGGCTTGAATACCAAG					
			9373 GGAAGAAGCAGCAGCCATGCTCAGAGTGAAGTGAAGTTCCTCAAGTTGGCCACAGCAGGTCA					
			137 GGAAGAAGCAGCAGCCATGCTCAGAGTGAAGTGAAGTTCCTCAAGTTGGCCACAGCAGGTCA					
			9433 ATGCCACATGATGACACAGTGGCGGTGAGTGCATCTTGCTGAACTTACCAAGAG					
			197 ATGCCACATGATGACACAGTGGCGGTGAGTGCATCTTGCTGAACTTACCAAGAG					
			9493 AAGATTTTCATCTCTTACTCCAGGTGATACAGATTAACAGGCGCTGTGGAGATCTTTATGA					
			257 AAGATTTTCATCTCTTACTCCAGGTGATACAGATTAACAGGCGCTGTGGAGATCTTTATGA					
			9553 ATAAATCAAGATGATCATCGGGCTTTAGATGGCCATGTCGTGTCAGAGTCCCGGGAG					
			317 ATAAATCAAGATGATCATCGGGCTTTAGATGGCCATGTCGTGTCAGAGTCCCGGGAG					
			9613 CCACCTTCATCTTACCAAGGCTCTGTCAAGGAGCCAGGCTTTGGGCAAGTTCGGCTTTCAA					
			377 CCACCTTCATCTTACCAAGGCTCTGTCAAGGAGCCAGGCTTTGGGCAAGTTCGGCTTTCAA					
			9673 GACTGAGCTCAGGCTGCTGAGATCAGACCCCGAGTCCATTTGGCGGCTTGGCTTCCA					
			437 GACTGAGCTCAGGCTGCTGAGATCAGACCCCGAGTCCATTTGGCGGCTTGGCTTCCA					

QY 9733 ACAGAGCTCAGTGGAGCGGAGTCTGTCCTTTCAATGCGCTTATTGAGGCT 9792
 DB 497 ACAGAGCTCAGTGGAGCGGAGTCTGTCCTTTCAATGCGCTTATTGAGGCT 556
 QY 9793 TCGTCTCATCTCTACAGCAGAGAGAGCCAAAGTCTTTCATAGCTATGCTG 9852
 DB 557 TCGTCTCATCTCTACAGCAGAGAGAGCCAAAGTCTTTCATAGCTATGCTG 616
 QY 9853 GCCAGAGAACCAATGTTGGGCCCATTTGAG 9887
 DB 617 GCCAGAGAACCAATGTTGGGCCCATTTGAG 651

RESULT 6
 CF744273 748 bp mRNA linear EST 10-OCT-2003
 LOCUS UI-M-GVO-clis-b-24-0-UI.r1 NIH_BMAP_GVO Mus musculus cDNA clone
 DEFINITION IMAGE:30620879 5', mRNA sequence.

ACCESSION CF744273
 VERSION CF744273.1 GI:37640612
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE NIH-MGC <http://mgc.nci.nih.gov/>.
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cgaabs-r@mail.nih.gov
 Tissue Procurement: Dr. James Lin, University of Iowa
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at
<http://genome.iowa.edu/distribution/mouseefl.html>
 This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

FEATURES
 source
 Location/Qualifiers
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 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE:30620879"
 /issue_type="whole brain"
 /lab_host="DH10B (T1 phage resistant)"
 /dev_stage="1,5, and 15 days newborn"
 /clone_1ib="NIH_BMAP_GVO"
 /note="Organ: Brain; Vector: pYX-Abs; Site_1: Bcor I; Site_2: Not I; The library was constructed according to Bernaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Abs vector. The library tag sequence located between the Not I site and the polyA tail is CGACTGAT. This library was created for the University Iowa Brain Anatomy Project (BMAP). 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemm Chin, Ph.D., program coordinator."

ORIGIN

Query Match 6.1%; Score 622; DB 7; Length 748;
 Best Local Similarity 90.1%; Freq. No. 2,4e-141;
 Matches 675; Conservative 0; Mismatches 73; Indels 1; Gaps 1;

QY 6835 CACCTCCAGGAGCGCGCTGAGAGCCACTGACAGTGTCTGACACAGGCTTATGAGCAAC 6894
 DB 1 CATCTCCAGGCGGGGTGCGAGGGCCACCGCAGAGTGTCTGATATCGGCTGTGGAGCAAC 60
 QY 6895 CGCAATGTCCACCAAGTGTGCTCTGTGACTTGTCTGATGTCAGTACATGACGCTG 6954
 DB 61 AGCAATGTCCCCCTCAAGTGTGCTCTGTGACTTGTCTGATGTCAGTACATGACGCTG 120
 QY 6955 GAGCATGGCCGATGAGGCTTATCTTTGAGACACAGTATGATGATGTCAGGCGGCTGATG 7014
 DB 121 GAGCAGGCGCGGTGAGGCTCATCTTGAGCCAGATGATGATGTCAGGCGGCTGATG 180
 QY 7015 CTCACTGTGACCCCTGCTACTATACCTGAGCCAAAGGATCATCCGCTGACGCCAAT 7074
 DB 181 CTCACTGTGACCCCTGCTACTATACCTGAGCCAAAGGATCATCCGCTGACGCCAAT 240
 QY 7075 GGCATATGAGGCTGTGGGAGCTTACGCGCCACTGCGGATCATCTCTGTGAGAGCTC 7134
 DB 241 GCGAGTGTGAGGCTGTGGGAGCTTACGCGCCACTGCGGATCATCTCTGTGAGAGCTC 300
 QY 7135 CGGATTCGCCCATGAGCGGACCGGATGAGGACATGTCGTCACGCGGCAAGCAGCATC 7194
 DB 301 CCACACCCCAAGTGTGACCGGATGAGGACATGTCGTCACGCGGCAAGCAGCATC 360
 QY 7195 TTCTCTGCAATTCGATACACACTGCTGAGGCTCCAGGATGCTGATGATGATGATGAT 7254
 DB 361 TTCTCTGCAATTCGATACACACTGCTGAGGCTCCAGGATGCTGATGATGATGATGAT 420
 QY 7255 GGGCTGTGAGTGTGCTGAGAGTCCGCTGCTTGTGAGCACTGTGGATCTCTGAGGCC 7314
 DB 421 GGACTGTGAGTGTGCTGAGAGTCCGCTGCTTGTGAGCACTGTGGATCTCTGAGGCC 480
 QY 7315 ATTGCAAGGACACATCAATGAGGAGAGAACTACAGCTACCGGGGAGTGTGATGACAA 7374
 DB 481 ATTGCAAGGACACATCAATGAGGAGAGAACTACAGCTACCGGGGAGTGTGATGACAA 540
 QY 7375 TGCAATGTGCTTCCGCTGATGCGCATGTCTGTGCGCATCTGCGCAGCAGATCATGAC 7434
 DB 541 TGCAAGGCTGTGCTTCCGCTGATGCGCATGTCTGTGCGCATCTGCGCAGCAGATCATGAC 600
 QY 7435 TGTGTGGGCAAGACCCCTTTCTGTGTGCGCATTTACTGTGACACCCAGGCAACCTGTG 7494
 DB 601 TGTGTGGGCAAGACCCCTTTCTGTGTGCGCATTTACTGTGACACCCAGGCAACCTGTG 659
 QY 7495 AACGCGCTCAGTCAAGGAGTAAACGATTTAACTCAAGATGTGTCAGATTTGTTGCAAC 7554
 DB 660 AACGCGCTCAGTCAAGGAGTAAACGATTTAACTCAAGATGTGTCAGATTTGTTGCAAC 719
 QY 7555 CCGTGGTATATGCTGAGGAGGCTGTG 7583
 DB 720 CNAAGATATATGCTGAGGAGGCTGTG 748

RESULT 7
 BX671124 673 bp mRNA linear EST 07-MAY-2004
 LOCUS BX671124 Sus Scrofa 1library (scac) Sus scrofa cDNA clone
 DEFINITION Bx600361.d.22 5prim, mRNA sequence.

ACCESSION BX671124 GI:37982337
 VERSION BX671124.1
 KEYWORDS EST.
 SOURCE Sus scrofa (pig)
 ORGANISM Sus scrofa

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. Bonnet,A., Tosser-Klopp,G., Benne,F., Cabau,C., Villiger,S., Soares,M., Bernaldo,F. and Hately,F. A pig Normalised Multi-Tissue cDNA Library Unpublished (2003)
 JOURNAL Contact: Tosser-Klopp G
 COMMENT Institut National de la Recherche Agronomique

Chemin de Borde-Rouge - Auzeville BP27, 31326 Caetanet-Tolosan cedex, FRANCE
 Tel: 33 (0) 5.61.28.51.14
 Fax: 33 (0) 5.61.28.53.08
 Email: toseer@toulouse.inra.fr
 Sequence cleaned of vector, adaptor and repetitions. Contact us at bigenassupport@jouy.inra.fr to obtain the chromatogram of this sequence.
 Plate: 0036 row: d column: 22.

FEATURES

Source

Location/Qualifiers

1. 673

/organism="Sus scrofa"

/mol_type="rRNA"

/db_xref="taxon:9823"

/clone="scac00361.d.22"

/tissue_type="mixed"

/clone_lib="Sus Scrofa library (scac)"

/note="Vector: pT713D-pac vector; tissues: adipose tissue, brain, kidney, liver, muscle, ovary, testis, heart, hypothalamus, pancreas, skin, spleen, thymus, placenta, pituitary gland, seminal vesicle, small intestine, uterus, adrenals, bulbo urethral gland, cerebral trunk, epididymis, female gonad, gall-bladder, hippocampus, large intestine, male gonad, melanocytes, stomach, udder"

ORIGIN

Query Match 5.5%; Score 558.6; DB 5; Length 673;
 Best Local Similarity 90.2%; Pred. No. 9.6e-126;
 Matches 609; Conservative 0; Mismatches 64; Indels 2; Gaps 1;

2559 TGTTCGAGTGTGGGAATCAGTCACAGGCACTCAGGTAAGTTCCTCCCACTT 2618
 1 TGTTCGAGTGTGGGAAT--AGTCACGGGCACTCAGGCACTTGTCTCCCACTT 58

2619 TCCTGTGAATCAATTAACAATCATGATCATCTCTCATCCAGCCAGCGGAA 2678
 59 TCCTGTGAATCAATTAACAACAAGATATCTCATCCAGCCAGCGGAA 118.

2679 GGGAAATTCAGTGAAGCCAGGCGATTCGAATCTCCGAGAGAGATCTCTCAAGTTA 2738
 119 GGGAAATTCAGTGAAGCCAGGCGATTCGAATCTCTCAAGAGAGATCTCTCAAGTTA 178

2739 TGATGGCAACAACAATCCGCGCTTGTGAGGAGTTTATGACCATTCAGATGATGG 2798
 179 CGATGGCAACAACAATCTCTCCGCTTGTGAGGAGCTTCAAGCGCTCCAGATGCTGG 238

2799 GGTGACTTTGAACAGCAATCCAGCACTGTGTGCTGATTTCACTCATGATCTGAAA 2858
 239 GGTGACTTTGAACAGCAATCCAGCACTGTGTGCTGATTTCACTCATGATCTGAAA 238

2859 CACGAGCAAGGCTTTGAATCTGCACTTTTTCAGCTTTGAATCAATGATGAGACC 2918
 299 CACGAGCAAGGCTTTGAATCTGCACTTTTTCAGCTTTGAATCAATGATGAGACC 358

2919 AGGACCCCCCAAGTTGGTACAAAGTTTCAATGATGATGATTTTTCAGGAGCTCCG 2978
 359 GGGACCCCCCAAGTTGGTACAAAGTTTTCAGTATGAGGCAATTTTTCAGGAGCTCCG 418

2979 GTCTTCAGCTGTGACCTTGATTAACAGCTTCGCGGATGATGAGAGAGCTGTGCTGAG 3038
 419 GTCTTCAGCTGTGACCTTGATTAACAGCTTCGCGGATGATGAGAGAGCTGTGCTGAG 478

3039 TGGAGAGCGCGGACCTTGAGGACCGGCTCTGCGCACTGTGTGCGGAGTGTGAGGAGAC 3098
 479 CGGAGAGCGGACCTTGAGGACCGGCTCTGCGCACTGTGTGCGGAGTGTGAGGAGAC 538

3099 AGTGAAGAGAGAGTGTGCGGAGCGGCTGTGCTGACCGCGGATTCAGCTCCATATGACA 3158
 539 AGTGAAGAGAGAGTGTGCGGAGCGGCTGTGCTGACCGCGGATTCAGCTCCATATGACA 598

3159 CAATCTCACTGATCTGACCAATCGAAGAGAGCGGCTGACCAATTTGGGCTACACTT 3218
 599 CAATCTCACTGATCTGATCTGACCAATCGAAGAGAGCGGCTGACCAATTTGGGCTACACTT 658

Qy 3219 CCTGTGTTTGACAC 3233
 Db 659 CCTGTGTTTGACAC 673

RESULT 8
 CF531622
 LOCUS
 DEFINITION
 CF531622 666 bp mRNA 1linear EST 12-SEP-2003
 UI-M-FY0-cgg-g-06-0-UI-r1 NIH_BMAP_FY0 Mus musculus cDNA clone
 IMAGE:30356213 5', mRNA sequence.
 CF531622
 VERSION
 CF531622.1 GI:34583590
 KEYWORDS
 EST.
 SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Dr. Jim Lin, University of Iowa
 cDNA library preparation: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/mouseefl.html>
 This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

Seq primer: pyx-5.

FEATURES

Source

Location/Qualifiers

1. 666

/organism="Mus musculus"

/mol_type="rRNA"

/strain="C57BL/6"

/db_xref="taxon:10090"

/clone="IMAGS:30356213"

/tissue_type="whole brain"

/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"

/lab_host="DH10B (T1 phage resistant)"

/clone_lib="NIH BMAP FY0"

/note="Organ: Brain; Vector: pyx-Asc; Site_1: Ecor I; Site_2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction. Ligated with Ecor I adaptor, digested with NotI and then cloned directionally into pyx-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGCGAGACAG. This library was created for the University of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemlin Chin, Ph.D., program coordinator."

ORIGIN

Query Match 5.4%; Score 546; DB 7; Length 666;
 Best Local Similarity 88.7%; Pred. No. 1.2e-122;
 Matches 591; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

8378 CTGGATTCAGGCATGAGCTTCGCGTGGGCAATGATTCAGGTACAAACAACCTGTGA 8437
 1 CTGGATTCAGGCATGAGCTTCGCGTGGGCAATGATTCAGGTACAAACAACCTGTGA 60

8438 CATATCAGTGTGTCTCTGCTATATGATGAGTCACTAAGATATCTGTGCTGAGCTGCA 8497
 61 CATATCAGTGTGTCTCTGCTATATGATGAGTCACTAAGATATCTGTGCTGAGCTGCA 120

OY	8498	CCAAAGACCGGACATGAGATGGAACCAAGCCCGTGTGGAAAGCTCATGTGCAAGCAC	8557
Db	121	CCMAGACCGGACCTTGAAACGTTACCAAGCCGGTTTGAAAGCTATCATGTGCAAACTTC	180
OY	8558	CTCCGCTCATCCCAATGGAGAGTGTGTGGGTCTGACTTCAATGTGGAGCTCAAGTGTGA	8617
Db	181	CTAGCTCATCCGAATGGAAAGTGTGGGTCGACTTCACTTCAAGTGGGCTCTAGCGTGA	240
OY	8618	CTTAATGCTGCTTGGAGGGGTAACACGCTCTCCCTGCCCCGGGTTCACCTGTGAGGGA	8677
Db	241	GCTAAGCCTGCTTGGAGGGATACACGCTCTCCCTGCGGTGCTCACCTGCGAGGGAA	300
OY	8678	ATGGTCCCTGGACCGGAGAGCTGCCTCAGTGTTCCTGTGTCTTGCGGGGATCCTGCT	8737
Db	301	ACGAGTCTTGAGCCGGAAGCTGCTCAGTGTTCCTCCGCTGTTCGCGGAACCCAGGGG	360
OY	8738	TCCGCTCCCTGTGGAGAGAGAGACCAAGGCTTCTCCTACAGGTCATCTGTCTCTCT	8797
Db	361	TCCCCCTCGAAGGAGAGAGAGACCGAGTTCTCCTACAGGTCATCTGTCTCTCT	420
OY	8798	CCTGCGCATCCCTCTGTGCTGTGTGGCTCTCCACGAGGTTTGGCAGTCAAGTGGGA	8857
Db	421	CCTGCGCAGCTCTCTGTGCTGTGGGCTCCCAAGAGTTTGGCAGTCAAGCGGA	480
OY	8858	CATGAGTGGGACCCAGCCACGCTGCAATGATCCGACCTTGACCAAGTGTGCGAACCTG	8917
Db	481	CGTAGAGTGGACACAGCCACGCTGCAATGATCCCAAGCTGACCAATGTCAAGTCTGTG	540
OY	8918	GTGTGCCACAGTTTGGGATACAGAACATTTCTCAGGGGTACACAGTTTGGAGACACAGTC	8977
Db	541	GCAATGCCCAATTGGAATACAGAACAGCTCCCAAGCTTAACAGTTTGGAGCACAGTGTC	600
OY	8978	TCTTCCGTTGTCAAAAAGGCTACCTGCTTCAAGGGCTCCACCAAGACCTGCTCCCAA	9037
Db	601	TATTCGGTTGTCAAAAAGGTTACCTGCTTCAAGGGATCCACCAAGACCTGCTTCCCA	660
OY	9038	ACCTGA 9043	
Db	661	ACCTGA 666	

RESULT 9	659 bp	mRNA	linear	EST 24-OCT-2001
BB309178				
LOCUS	BB309178			
DEFINITION	BB309178 RIKEN full-length enriched, adult male corpora quadrigemina Mus musculus cDNA B230309H23, mRNA sequence.			
ACCESSION	BB309178			
VERSION	BB309178.2			
KEYWORDS	GI:16402481			
SOURCE	EST.			
ORGANISM	Mus musculus (house mouse)			
	Mus musculus			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclirognathi; Muridae; Murinae; Mus.			
REFERENCE	1 (bases 1 to 659)			
AUTHORS	Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hizumoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,U., Komno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sasaki,C., Sasaki,K., Sano,H., Sasaki,D., Shibata,K., Shingawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toyu,T., Muramatsu,M. and Hayashizaki,Y.			
TITLE	RIKEN Mouse ESTs (Arakawa,T., et al. 2001)			
COMMENT	Unpublished (2001)			
	On Jul 10, 2000 this sequence version replaced gi:9009883.			

Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Saitama-cho, Tsukuba-shi, Ibaraki 305-3858, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: resgsc.riken.jp, URL:http://genome.gsc.riken.jp/
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,

FEATURES

Itoch.M., Komno.H., Okazaki.Y., Muramatsu.M. and Hayashizaki.Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. *Genome Res.* 10 (10), 1617-1630 (2000)
wagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Matahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
Matsura,S., Kawai,J., Okazaki,Y., Muramatsu.M., Inoue,Y., Kira,A.
and Hayashizaki.Y.
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer. *Genome Res.*
10 (11), 1757-1771 (2000)
Komno,H., Fukunishi.Y., Shibata,K., Itoh.M., Carninci,P.,
Sugahara.Y. and Hayashizaki.Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. *Genome Res.* 11 (2), 281-289 (2001)
Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamamata,I.,
Aizawa,K., Fukuda,S., Hara,A., Itoh.M., Kawai,J., Shibata,K. and
Hayashizaki.Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences *Mamm. Genome* 12, 673-677 (2001)
Please visit our web site (<http://genome.gsc.riken.go.jp/>) for
further details.
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Location/Qualifiers

```
FEATURES  
SOURCE  
  
location/Qualifiers  
1 .659  
/organism="Mus musculus"  
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/_dev_stage="adult"  
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_note="Site 1: SalI; Site 2: BamHI; cDNA library was  
prepared and sequenced in Mouse Genome Encyclopedia  
Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in  
RIKEN. Division of Experimental Animal Research in Riken  
contributed to prepare mouse tissues. 1st strand cDNA was  
primed with a primer [5'.  
GAGAGAGAAGATCCACAGCGCTTTTTTTTNN 3', cDNA was  
prepared by using trehalose thermo-activated reverse  
transcriptase and subsequently enriched for full-length by  
cap-trapper. cDNA went through one round of normalization  
to Rot = 20.0 and subtraction to Rot = 459.0. Second  
strand cDNA was prepared with the primer adapter of  
sequence [5' GAGAGAGAATTTCGGATTAAATAAATTAATCCCCCCCCCC  
3', cDNA was cleaved with XhoI and BamHI. Vector: a  
modified bluescript KS(+) after bulk excision from Lambda  
FLC I."`
```

[illegible]

Db	127	AAGCAAGACGATTGAGTCGCTCGTAAGAGACCTCTCGAAGGTCTATGACGGCACTAACA	186
Qy	2753	ACTCCGCCCGCTTTGCTGGAGATTTTAAACCATTCTGAGATGATGGGGGTGACTTTGAACA	2812
Db	187	ACTCGCCCCGTTTGTGTGGGGGCTTTCACACCGCTCTGAGATATTTGGGGGTGACTTTGAACA	246
Qy	2813	GCACATCCAGCAGTGTGTGGCTTGATTTTCATCATCAGTAGTGTGAAAAACACGACAAGGCT	2872
Db	247	GCACTCTAGCAGCTTTGTGGCTTGACTTCAATCACAGATGTCAGAAAAACACGACAAGGCT	306
Qy	2873	TTGAACTGCACTTTTCCAGCTTTGAACTCATCAAAATGTAGAGACCAGAAACCCCAAGT	2932
Db	307	TTGAACCTTCAGTTCCTCTAGTTTCGAGCTCAATCCGATGTGAGAGACCCAGGACCCACAGT	366
Qy	2933	TTGGCTACAGGTTTATGATGAAAGTCAATTTTGCAGGGAGCTCCGTGCTTTCAGCTGTG	2992
Db	367	TCGGCTACAGGTTTACATGAGAGGTCAATTTTGCAGGGAGCTCCGTGACCTTTCAGCTGTG	426
Qy	2993	ACCCTGATACAGCCTGCGGGGTAGTAGAGAGCTGCTGTCTGATGTGAGAGCGCCGGA	3052
Db	427	ACCCTGCTACAGTCTTTCGGGGCAGTAGAGAACTATGTGCTCTGATGTGTAAACGACAGA	486
Qy	3053	CCTGGGACCGGGCTCTGGCCACCTGTGTGCGCGAGTGTGAGAGGACAGTAGAGAGAGG	3112
Db	487	CGTGGACCGACCGCTGCCAACCTGTGTGCTGATGTGAGAGGGACAGTAAAGAGAGGG	546
Qy	3113	TGTGGGGCAGGTGCTGTCAACCCGGGATTCAGACTCCCTATGAACACATCTCAACTGCA	3172
Db	547	TGTCAAGGACAGGTGTGCTGTGCCCCGGGTACCGGCTCCTATGAACACATCTCAACTGCA	606
Qy	3173	TCTGGACCATGGAAGCAGAGCCGGGCTGCACCATTTGGG	3210
Db	607	TCTGGACCATGGAAGCAGAGCCGGGCTGCACCATTTGGG	644

RESULT	10
LOCUS	AK046385
DEFINITION	Mus musculus adult male corpora quadrigemma cDNA, RIKEN full-length enriched library, clone:B230378I17 product:hypothetical Sushi domain / SCR repeat / CDP module/ CUB domain containing protein, full insert sequence.
ACCESSION	AK046385
VERSION	AK046385.1 GI:26091501
KEYWORDS	HTC; CAP trapper.
SOURCE	Mus musculus (house mouse)
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1 Carninci,P. and Hayashizaki,Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999) 99279253
JOURNAL MEDLINE	10349636
PUBLISHED	2
REFERENCE	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Komoto,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000) 20499374
JOURNAL MEDLINE	11042159
PUBLISHED	3
REFERENCE	Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Komoto,H., Akiyama,J., Nishi,K., Kitunaka,T., Tashiro,H., Itoh,M., Suni,N., Ishii,Y., Nakamura,S., Hazama,M., Nishino,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Matsubiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multipicapillary sequencer
TITLE	

JOURNAL
MEDLINE
PMID
11076861

4
The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)

JOURNAL
REFERENCE
AUTHORS

TITLE
The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

JOURNAL
REFERENCE
AUTHORS

TITLE
Adachi, J., Alizawa, K., Akinura, T., Arakawa, T., Bono, H., Carninci, P., Fukushima, S., Furuno, M., Hanagasaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T., Horii, F., Imomani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katch, H., Kawai, J., Kojima, Y., Kondo, S., Komori, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Niyazaki, R., Ohno, M., Ohata, N., Okazaki, Y., Saito, R., Saitoh, K., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Saeki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-ree@gsc.riken.jp).
URL: http://genome.gsc.riken.jp/.
Fax: 81-45-503-9216

COMMENT
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in RIKEN Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/.
URL: http://fantom.gsc.riken.jp/.
Location/Qualifiers
1..2841
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM.DB:B230378117"
/db_xref="taxon:10090"
/clone="B230378117"
/sex="male"
/tissue type="corpora quadrigemina"
/clone_id="RIKEN full-length enriched mouse cDNA library"
/dev stage="adult"
1..2841
/note="hypotheetical Sushi domain / SCR repeat / CDP module/ CDS domain containing protein (InterPro|IPR000436, evidence: InterPro)"

FEATURES
SOURCE

ORIGIN

Query Match 5.1%; Score 513.4; DB 3; Length 2841;
Best Local Similarity 76.1%; Pred. No. 1.9e-114;
Matches 699; Conservative 0; Mismatches 136; Indels 84; Gaps 2;

DB 1047 GGCCTTACGCGCCAGTACCAAGTCAAGAGCAAGTGAAGTCTCGAGGTGAAG 144
145 CTGATGCCCGAAGACACAGCCAGAAAGCGTCTGTGTTAACTCAGGTTGGTGTGCC 204
DB 1107 CTGATGCCCGAAGACCAATTAACCAAGACATCTGTGTTAACTCAGGTTGGTGTGCC 1166

ORIGIN

RCB-0526 Jyg-MC(A) cDNA"

Query Match 4.5%; Score 458.4; DB 6; Length 656;
Best Local Similarity 86.7%; Pred. No. 4.5e-101;
Matches 504; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

4880 GAACAAACCGGCTGCTGCTTCTGACAGACCCCAACGCTCTACCTTCACTTCTACT 4939
DB 76 GAACGACAGTACCGGCTTCTGACAGACCCCAACGCTCTACCTTCACTTCTACT 135
4940 CAGATATCAGCGTATCTGACAGTCTGCTTCTGACAGACCCCAACGCTCTACTGAGA 4999
DB 136 CTGACATCAGTGTGTCTGCTGCTGCTTCTGACAGACCCCAACGCTCTACTGAGA 195
5000 GTTGTCCGGAACCTGCTGCTGCTGCTTCTGACAGACCCCAACGCTCTACTGAGA 5059
DB 196 GTTGTCCGGAACCTGCTGCTGCTTCTGACAGACCCCAACGCTCTACTGAGA 255
5060 ATGATGTGTGTCTTCTGACAGACCCCAACGCTCTACTGAGA 5119
DB 256 ACACGCTGTCTTCTGACAGACCCCAACGCTCTACTGAGA 315
5120 CCTGATGCGCGGACAGTCTGCTGCTTCTGACAGACCCCAACGCTCTACTGAGA 5179
DB 316 CCTGATGCGCGGACAGTCTGCTGCTTCTGACAGACCCCAACGCTCTACTGAGA 375
5180 GTGGGGGAAACAGTGAAGAGATGGAAGAGGAGTCTGAGACCCCGGCTTCCAGCAACT 5239
DB 376 GTGGGGGAAACAGTGAAGAGATGGAAGAGGAGTCTGAGACCCCGGCTTCCAGCAACT 435
5240 ACCCGAGTAAACAGTGAAGAGATGGAAGAGGAGTCTGAGACCCCGGCTTCCAGCAACT 5299
DB 436 ACCCGAGTAAACAGTGAAGAGATGGAAGAGGAGTCTGAGACCCCGGCTTCCAGCAACT 495
5300 TCCAGTCTCTGAACTTCTGACAGACCCCAACGCTCTACTGAGA 5359
DB 496 TCCAGTCTCTGAACTTCTGACAGACCCCAACGCTCTACTGAGA 555
5360 CCTATGAGACAGCGCGATGATGGAAGATGGAAGAGGAGTCTGAGACCCCGGCTTCCAGCAACT 5419
DB 556 CCTATGAGACAGCGCGATGATGGAAGATGGAAGAGGAGTCTGAGACCCCGGCTTCCAGCAACT 615
5420 TCTCCAGTCTCTGAACTTCTGACAGACCCCAACGCTCTACTGAGA 5460
DB 616 TCTCCAGTCTCTGAACTTCTGACAGACCCCAACGCTCTACTGAGA 656

RESULT 12
BX676029 671 bp mRNA linear EST 07-MAY-2004
LOCUS BX676029 Sus Scrofa library (scac) Sus scrofa cDNA clone
DEFINITION scac00361.d.22 3prim, mRNA sequence.
ACCESSION BX676029
VERSION BX676029.1 GI:38010164
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
1 (bases 1 to 671)
Bonnef, A., Tosser-Klopp, G., Benne, F., Cabu, C., Villedier, S.,
Soares, M., Bonaldi, F. and Haley, F.
A Pig Normalised Multi-Tissue cDNA Library
Unpublished (2003)
Contact: Tosser-Klopp G
Genetique Animale
Institut National de la Recherche Agronomique
Chemin de Borde-Rouge - Auzeville BP27, 31326 Castanet-Tolosan
cedex, FRANCE
Tel: 33 (0) 5.61.28.51.14
Fax: 33 (0) 5.61.28.53.08
Email: tosser@toulouse.inra.fr

FEATURES

Sequence cleaned of vector, adaptor and repetitions. Contact us
at sigenastupport@jouy.inra.fr to obtain the chromatogram of this
sequence.
Plate: 0036, row: d column: 22.
Location/Qualifiers
1..671
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="scac00361.d.22"
/tissue_type="mixed"
/clone_lib="Sus Scrofa library (scac)"
/note="Vector: pT7T3D-pac vector; tissues: adipose tissue,
brain, kidney, liver, muscle, ovary, testis, heart,
hypothalamus, pancreas, skin, spleen, thymus, placenta,
pituitary gland, seminal vesicle, small intestine,
uterus, adrenals, bulbo urethral gland, cerebral trunk,
epididymus, female gonad, gall-bladder, hippocampus,
large intestine, male gonad, melanocytes, stomach, udder"

ORIGIN

Query Match 4.5%; Score 453.2; DB 5; Length 671;
Best Local Similarity 92.6%; Pred. No. 8.6e-100;
Matches 476; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

5177 AGTGGGGGAAACAGTGAAGAGATGGAAGAGGAGTCTGAGACCCCGGCTTCCAGGCA 5236
DB 1 AGTGGGGGAAACAGTGAAGAGATGGAAGAGGAGTCTGAGACCCCGGCTTCCAGGCA 60
5237 ACTACCCAGTAAACAGTGAAGATGCTCTGGAAGAAATGACATGCGCGGCTTGGAGCTC 5296
DB 61 ACTACCCAGTAAACAGTGAAGATGCTCTGGAAGAAATGACATGCGCGGCTTGGAGCTC 120
5297 ACATCCAGTCTCTGAACTTCTGACAGACCCCAACGCTCTACTGAGA 5356
DB 121 ACATCCAGTCTCTGAACTTCTGACAGACCCCAACGCTCTACTGAGA 180
5357 GCCCGATGAGACAGCGCGATGATGGAAGATGGAAGAGGAGTCTGAGACCCCGGCTTCCAGCAACT 5416
DB 181 GCCCGATGAGACAGCGCGATGATGGAAGATGGAAGAGGAGTCTGAGACCCCGGCTTCCAGCAACT 240
5417 TCTCTCCAGTCTCTGAACTTCTGACAGACCCCAACGCTCTACTGAGA 5476
DB 241 TCTCTCCAGTCTCTGAACTTCTGACAGACCCCAACGCTCTACTGAGA 300
5477 CAGGATTCAGCTGAGATTCAGAGCTTGAATTCAGAGTGGCCAGACCCAGAGCCCT 5536
DB 301 CAGGATTCAGCTGAGATTCAGAGCTTGAATTCAGAGTGGCCAGACCCAGAGCCCT 360
5537 TTGCCAATGGCATTTGAGAGGAGAGCTGGCTTAAACGTTGGAGATGAGAT 5596
DB 361 TTGCCAATGGCATTTGAGAGGAGAGCTGGCTTAAACGTTGGAGATGAGAT 420
5597 GCCTCCCGGGGTATCAATTGAGTGGCCACCTGTCTCTCAGTGTCAACATGGCAACCAAC 5656
DB 421 GCCTCCCGGGGTATCAATTGAGTGGCCACCTGTCTCTCAGTGTCAACATGGCAACCAAC 480
5657 GGAATGGGACCAACCCCTGCTCCCAAGTGAAGT 5690
DB 481 GGAATGGGACCAACCCCTGCTCCCAAGTGAAGT 514

RESULT 13
BU370222 733 bp mRNA linear EST 28-NOV-2002
LOCUS BU370222 603595935F1 CSBQCHN73 Gallus gallus cDNA clone CHEST5639 5', mRNA
DEFINITION sequence.
ACCESSION BU370222
VERSION BU370222.1 GI:25878223
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

REFERENCE 1 (bases 1 to 733)
Boardman, P. E., Sanz-Ezquerro, J., Overton, I. M., Burr, D. W., Bosch, E., Fong, W. T., Tickle, C., Brown, W. R., Wilson, S. A. and Hubbard, S. J.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)

JOURNAL MEDLINE 2235534
PUBMED 12445392

COMMENT Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology (UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers

FEATURES source
1..733
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Compton line 151"
/db_xref="taxon:9031"
/clone="CHEST563e9"
/sex="Female"
/tissue_type="not cerebrum or cerebellum"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="CSEQC/N73"
/note="Organ: brain; Vector: pBluescript II KS(+); Site_1: EcoRI; Site_2: NotI; This normalized library was constructed from 1 million independent clones. cDNA methylation was initiated using an oligo(dT) primer, using following this first strand reaction, double-stranded cDNA was bluntended, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., RNAs (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996) 791, except that a significantly longer reannealing hybridization was used."

ORIGIN

Query Match 4.4%; Score 444.2; DB 5; Length 733;
Best Local Similarity 78.0%; Pred. No. 1.5e-97;
Matches 572; Conservative 0; Mismatches 158; Indels 3; Gaps 3;

8365 AACTGTGATGACCTGGGATTCAGGCAATGCGCTGGGCAATGACTTCAGGTAC 8424
2 AACTCGGTGACCCAGGTGTGCGACGCAACGCGATTAGCTGGGCAATTTTACCTAC 61

8425 AACAAAGTGTGACATATCATGCTGTCTCCGTGCTATGATGAGAGTCAATAGATATCT 8484
62 AACAAAGTGTGATGCTGTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 121

8485 GTGCTGAGTGTGACCAAGGACCGGACATGAGTGAACCAACCCGCTGTGCAAACTCTC 8544
122 TCTGTGATGTGTACAAAGACCGAACCTGGAATGGAACCAACCTGCGCAAACTCTATC 181

8545 ATGTGCAAGCCACTCCGCTCATCCCAATGGGAAGTGTGGGCTGTGATCTTCAATGTCG 8604
182 ATCTGTAAACCCCAACCAACCATCCCAATGCAAGTGTGGCTCGGATTTTCAGCTGG 241

8605 GGCTCAAGTGTATCTTATGCTGCTGTGAGGGGTATCAAGCTCTCCCTGCGCGGTGTTC 8664
242 GGCTCAAGTGTATCTTATGCTGCTGTGAGGGGTATCAAGCTCTCCCTGCGCGGTGTTC 301

8665 ACCTGTGAGGGAATGAGTGTGAGACCGGACGCTGCTCACTGTCTTCCCTGTGTTCGC 8724
302 ACCTGTGAGGGAATGAGTGTGAGACCGGACGCTGCTCACTGTCTTCCCTGTGTTCGC 361

8725 GGGATCTGTGATGCTCCGCTCCGCTGGAGAGAGAGACCGAGCTTCTCTACAGGTCA 8784
352 GGAATTCAGG-ATTCCTGCCCCAGGCGCGGGAGAGACCGAGCTTACAGTCCGCTCC 420

8785 TCTGTCTCTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 8844
421 TCTGTGCTCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480

8845 CAGTCATGTGAGACATGAGTGTGAGACCGGACCGGACCGGACCGGACCGGACCGGACCGG 8904
481 CAGTCATGTGAGTGTGAGTGTGAGACCGGACCGGACCGGACCGGACCGGACCGGACCGG 540

8905 TGTGAGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 8964
541 TGTGAGACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600

8965 GGAGACACATGCT 9024
601 GGAGACATGATTTTCTTCAAGTGCAGAGAGGGTAACT-CTGACAGGCTCCACCA-CAAG 658

9025 ACTGCTCTCCCAACCTGACCTGAGTGTGAGAACCCCACTGATGTGTCTCCCACTGCTGC 9084
659 ACTGCTCTCCCAACCTGACCTGAGTGTGAGAACCCCACTGATGTGTCTCCCACTGCTGC 718

9085 AGGACCCAGAGA 9097
719 AAGCAGCTGAAA 731

RESULT 14
A1928999
LOCUS
DEFINITION ausb10.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2519011 5' similar to SW:BNP1.MOUSE P98063 BONE MORPHOGENETIC PROTEIN 1 PRECURSOR ; mRNA sequence.
A1928999
A1928999.1 GI:5664963
EST.

ACCESSION A1928999
VERSION A1928999
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 458)
Hillier, L., Allten, M., Bowles, J., Dubuque, T., Geisel, G., Jost, S., Martin, J., Moore, B., Scheinberg, K., Sefton, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: eest@wustl.wustl.edu
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40RP from Glbco
High quality sequence stop: 429.
Location/Qualifiers

FEATURES source
1..458
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2519011"
/sex="male"
/tissue_type="frontal lobe"
/dev_stage="5 months post-conception"
/lab_host="DH10B"
/clone_lib="Schneider fetal brain 00004"
/note="Organ: brain; Vector: pBluescript SK (Stratagene); Site_1: SstI; Site_2: XhoI; Double-stranded cDNA was prepared from human fetal brain tissue. 5' and 3'

adaptors were used in cloning as follows: 5' adaptor sequence:
5'-GAGAGAGAGAGAGCTCAGAGATCCTTAATTAATTAATATCCCCCCCC-3'
and 3' adaptor sequence:
5'-GAGAGAGAGAGCTCAGAGATTTTTTTTTTTTTTT-3'. The library was size-selected for >0.5 kb inserts and has an average insert size estimated at 1.2 kb. This library was constructed using the CAP-trapper method for full-length enrichment and has not undergone amplification. Library was constructed by Dr. Claudio Schneider (UNCIB-Area Science Park, Trieste, Italy)."

ORIGIN

Query Match 4.3%; Score 440; DB 1; Length 458;
Best Local Similarity 99.8%; Pred. No. 1.4e-96;
Matches 451; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 5560 GCTGGCTACACGTCGGACATCATGACCTTGAGTCCCTCCGGGATCAATTGACT 5619
DB 7 GCTGGCTACACGTCGGACATCATGACCTTGAGTCCCTCCGGGATCAATTGACT 66
QY 5620 GGGCACCCTCTCTCTCACTGATCAATGACCAACCGGAATGGACACCCCTGGCC 5679
DB 67 GGGCACCCTCTCTCTCACTGATCAATGACCAACCGGAATGGACACCCCTGGCC 126
QY 5680 AAGTGTGAAGTCCCTCTGCGGGAACATCATCTTCCAAAGGCACTGTACTCCCG 5739
DB 127 AAGTGTGAAGTCCCTCTGCGGGAACATCATCTTCCAAAGGCACTGTACTCCCG 186
QY 5740 GGGTTCCTTAGCCCTGAC-TCCAGCTCCAGAGCTGTCTGCTGATCAACCGTGCAT 5798
DB 187 GGGTTCCTTAGCCCTGAC-TCCAGCTCCAGAGCTGTCTGCTGATCAACCGTGCAT 246
QY 5799 TGGCCATGGGTCTCCGCTCACTCACTGCTGACAGACAGAGCCCTTGGAGATTTCAT 5858
DB 247 TGGCCATGGGTCTCCGCTCACTCACTGCTGACAGACAGAGCCCTTGGAGATTTCAT 306
QY 5859 CACCATCTGGGATGGGCGCAACAGACAGACAGCGCTGGGCTTTCACCCGGAGCAT 5918
DB 307 CACCATCTGGGATGGGCGCAACAGACAGACAGCGCTGGGCTTTCACCCGGAGCAT 366
QY 5919 GGGCAAGAAAACAGTGCAGATTTCATCAACAGAGCTCTGCTCAAGTTCACCGTAGTC 5978
DB 367 GGGCAAGAAAACAGTGCAGATTTCATCAACAGAGCTCTGCTCAAGTTCACCGTAGTC 426
QY 5979 AGCCACAGGGGGATCTTCCCATAGCTTCT 6010
DB 427 AGCCACAGGGGGATCTTCCCATAGCTTCT 458

RESULT 15
CK12578 707 bp mRNA linear EST 01-MAR-2004
LOCUS SB02035A2B11.f1 normalized Keck-Tagu Library SB02 Taeniolypgia
DEFINITION gutata cDNA clone SB02035A2B11.f1 5, mRNA sequence.
ACCESSION CK12578
VERSION CK12578.1 GI:44822152
KEYWORDS EST.
SOURCE Taeniolypgia gutata
ORGANISM Taeniolypgia gutata
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Passeriformes; Estrifididae;
Estrifidinae; Taeniolypgia.
1 (bases 1 to 707)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
The Sordbird Neurogenomics Initiative: An Evolving Public Resource
for Study of Genes, Brain, and Behavior
Unpublished (2004)
Contact: David F. Clayton
University of Illinois
B107 CLSL, 601 S. Goodwin, Urbana, IL 61801, USA

Tel: 217 244 3668
Fax: 217 244 1648
Email: dclayton@uiuc.edu
Base Calling/Quality Scores: PHRED from Washington University
Genome Center.
Vector Trimming: Cross match from Washington University Genome
Center PHRAP suite. Low quality bases (Phred score < 20) were
trimmed from both ends of the sequence by an in-house script.
This sequence is vector free and at least 200 bp in length. Funded
by PHS grant # R01 NS045264, 'Sordbird Neurogenomics Initiative'.
PCR Primers
FORWARD: TAATACACTCACTATAGG3 (77)
BACKWARD: ATTACCTCACTAAG (73)
Insert Length: 707 Std Error: 0.00
Plate: SB02035A2 row: B column: 11
Seq primer: TAATACACTCACTATAGG3 (77)
High quality sequence stop: 707.
Location/Qualifiers
1..707
/organism="Taeniolypgia gutata"
/mol_type="mRNA"
/db_xref="taxon:59729"
/db_xref="SB02035A2B11.f1"
/issue_type="brain"
/dev_stage="late embryo, post-hatch days 1, 10, 20, 45,
and adult (pooled)"
/lab_host="DH10B"
/clone_lib="normalized Keck-Tagu Library SB02"
/note="Organ: brain; Vector: PHS II SK(+); Site 1:
ECORI(5' side of insert); Site 2: NotI (3' side of
insert); The library was constructed and normalized as
described by Bonaldo, M.F., Lennon, G. and Soares, M.B.
(1996), Genome Research 6(9): 791-806. An identifying tag
was added at the 3' during cDNA synthesis:
insertAAAAAAAAAAAAAAAAAATCCGA."

FEATURES

source

ORIGIN

Query Match 4.2%; Score 426.8; DB 7; Length 707;
Best Local Similarity 79.1%; Pred. No. 2.8e-93;
Matches 503; Conservative 0; Mismatches 133; Indels 0; Gaps 0;

QY 4538 GGGCCATCTCTCCGCTTCAATGATCACTCCGCTATGCTGACAGGGGTCGCCAGATGCG 4597
DB 1 GGGCCNNNNNGCCCTTCAATGATGACGCCCGCTACGCGCTCGAGGCTCCCTGCCATCC 60
QY 4598 AGTGCCTCCCTGTGCTGCGGCTTGGCCCAATGATGATCTTCAAGCCGCCAGCTGTGCG 4657
DB 61 AGTGCCTGACATGCGCGGCGCTTGGCAAGTGAATCTTCCGCCCACTGCGTGG 120
QY 4658 TGGCTGTGAGGCACTCAACAGAGAGCGAGGCGCACTCTGTCTCCCTGCTTCCAG 4717
DB 121 TGGCTGTGAGGCGGAGCACTGACGAGAGAGAGAGCACTCTGTCTCCAGGCTTCCG 180
QY 4718 AGCCGATCTCAACAGCTCACTGCTGTGAGAGATGCTGCGCCGAGAGGCTGGCA 4777
DB 181 AGCCGATCTCAACAGCTCACTGCTGTGAGAGATGCTGCGCCGAGAGGCA 240
QY 4778 TCCAGATCAAGTTGTCACTTTTGTGACAGAGCAAGTGGACCTGCTGGAATTTG 4837
DB 241 TCCAGATCAAGTTGTCACTTTTGTGACAGAGCAAGTGGATTCCTGGAATTTG 300
QY 4838 ATGTGCAATTAACATGTAACATCTGTGGAGATTCTCAGAACACCGTCTGCC 4897
DB 301 ATGTGCAATTAACACAGCACCATGCTGGGAGCTTCTGTGAACACAGTCTGCC 360
QY 4898 TTCTGAACGACCTTCAACAGCTTACCTTCACTTCTACTAGATCAGGATTCG 4957
DB 361 TTCTGAACGACCTTCAACAGCTTATCTGATTTCTATTCGATCAGGCTTCCG 420
QY 4958 CAGCTGCTTCACTTGAATCAAAACGATGGGCTGACAGATTTCGGAACCTGCTG 5017
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GenCore version 5.1.6
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OM nucleic - nucleic search, using SW model

Run on: October 18, 2004, 10:04:46 ; Search time 27137 Seconds
(without alignments)
17663.279 Million cell updates/sec

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Perfect score: 10136
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Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues
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Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

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13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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ACCESSION	AX685957.1	GI:29371852			
VERSION					
KEYWORDS					
SOURCE					
ORGANISM	Homo sapiens (human)				
REFERENCE					
AUTHORS	1 Alsobrook II, J.P., Anderson, D.W., Burgess, C.E., Boldog, F.L., Casman, S.J., Coleman, S.D., Edinger, S.R., Ellerman, K., Gerlach, V., Gorman, L., Grose, W.M., Guo, X., Herrmann, J.L., Kexda, R., Lepley, D.M., Li, L., Macdougall, J.R., Miller, I., Pena, C.E., Peyman, J.A., Rastelli, L., Rieger, D.K., Shimkets, R.A., Smithson, G., Spylek, K.A., Stone, D.J., Tchernev, V.T., Vernet, C.A., Voss, E.Z., Zehnuzen, B.D., Zhong, H. and Zhong, M.				
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ORIGIN					
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Best local Similarity	100.0%; Pred. No. 0;				
Matches 10136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
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DB	1 ATGGCGGGGCGCCCTCCCGCGCTTGGCTGCTGCTGAGTTGATCTCAAGCTGCTGT	60			
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5761 AGCTCCCAAGCTGTGTCTGCTGATCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5820
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ORIGIN

Query Match Best Local Similarity 86.0%; Score 8718.6; DB 9; Length 13113;

Matches 9389; Conservative 0; Mismatches 94; Indels 574; Gaps 4;

QY 101 AGCTAGTCAAGAAGCAATTGAGTTGAGTCTGAGGTGAGAGTATGCCCCAGCAAG 160
DB 937 ACCAAGTCAAGAAGCAAAATTGAGTTGAGTCTGAGGTGAGAGTATGCCCCAGCAAG 996
QY 161 ACAACAGCCAGAAGAGCTGTGTCTTAATCACTGAGTTGCTGTCTCCAGAGCATATATGT 220
DB 997 ACAACAGCCAGAAGAGCTGTGTCTTAATCACTGAGTTGCTGTCTCCAGAGCATATATATGT 1056
QY 221 GTCCAGACCTGGCATACCCGAAAGGGGCAAAAGACTAGGCTCGAGTTTCAAGTTAGAT 280
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QY 281 CCAGCGTCCAGTTCACTGCAACGAGGCTATGACCTGCAAGGCTCCAGCGGATCACTT 340
DB 1117 CCAGCGTCCAGTTCACTGCAACGAGGCTATGACCTGCAAGGCTCCAGCGGATCACTT 1176
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DB 1513 GGTCTCTTCCAGACTGATGAG 1572
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Db 4393 TCAATCTTCAACAAATTAACCAAGACCTTCAAGGCGCAAGAGAGTGTGAAGTGAAG 4452
Qy 3701 TGACCGTCTCAACAGACTTACAGTCCGCTGTGATTTAAATCATCTTAACTTGAAGCTG 3760
Db 4453 TGACCGTCTCAACAGACTTACAGTCCGCTGTGATTTAAATCATCTTAACTTGAAGCTG 4512
Qy 3761 GCTATGACTTTCCTCATATCTAAGACGAGGAGCTCTCAGCCCTCTCATATGAAGCT 3820
Db 4513 GCTATGACTTTCCTCATATCTAAGACGAGGAGCTCTCAGCCCTCTCATATGAAGACT 4572
Qy 3821 TCTATGCTTCCAGCTCCAGAGCGCATTTGAAGCAGACGACGACTCTTCTCGGCT 3880
Db 4573 TCTATGCTTCCAGCTCCAGAGCGCATTTGAAGCAGACGACGACTCTTCTCGGCT 4632

OY	3881	CCGACAGGAGACGACATCTGTGAGCAATGCTGGCTTCATCTATGACATTAACAGAAACCGC	3940
Db	4633	TCCGACGGAATGACATCTGTGACAAATGCTGGCTTCATCTATGACATTAACAGAAACCGC	4692
OY	3941	GGGAGTCATGTTTGTGATCCTGATTCATATCAAGAAACGACACGGGTGGGTCCGACCTGA	4000
Db	4693	GGGAGTCATGTTTGTGATCCTGATTCATATCAAGAAACGACACGGGTGGGTCCGACCTGA	4752
OY	4001	AGCTGGGCTCCTCCGTCACTACTACGCGAGGCTACAGAAATTGAGGGCACCTCGA	4060
Db	4753	AGCTGGGCTCCTCCGTCACTACTACGCGAGGCTACAGAAATTGAGGGCACCTCGA	4812
OY	4061	CCCTGAGCTGCATCCTGGGGCTGATAGGGAAACCCGTGTGGAAACAATCCCGGCAATCT	4120
Db	4813	CCCTGAGCTGCATCCTGGGGCTGATAGGGAAACCCGTGTGGAAACAATCCCGGCAATCT	4872
OY	4121	GCACAGCCCCCTGTGGGGGACAGTATGTGGGTTGGAAACGAGAGTGATCTTGCCCCCACT	4180
Db	4873	GCACAGCCCCCTGTGGGGGACAGTATGTGGGTTGGAAACGAGAGTGATCTTGCCCCCACT	4932
OY	4181	ACCCCCAGAACTACACAGTGAACAGATCTGCTGTATTTTGTATCTGTGCCAAGAACT	4240
Db	4933	ACCCCCAGAACTACACAGTGAACAGATCTGCTGTATTTTGTATCTGTGCCAAGAACT	4992
OY	4241	ATGTGTGTTTGGCCAGTTTCGCTTTCTTCAACAGGCCCTCAACAGACGTGTGAGGTTTC	4300
Db	4993	ATGTGTGTTTGGCCAGTTTCGCTTTCTTCAACAGGCCCTCAACAGACGTGTGAGGTTTC	5052
OY	4301	ACGACGGGCAACAGCCAGACATCGGGGGCTCCAGTCCCTCTGGGGGCTCCCATACAGAG	4360
Db	5053	ACGACGGGCAACAGCCAGACATCGGGGGCTCCAGTCCCTCTGGGGGCTCCCATACAGAG	5112
OY	4361	AATCACTGCCCTTGCCCACTTCATCAATCAAGTTCTCATTAAGTTACGCGCCAAAGCCTCG	4420
Db	5113	AATCACTGCCCTTGCCCACTTCATCAATCAAGTTCTCATTAAGTTACGCGCCAAAGCCTCG	5172
OY	4421	CACCAACAGAGGCTTCCACTTTGTCTACAGCGGTTCTTGAAACAGCGCCACGCACT	4480
Db	5173	CACCAACAGAGGCTTCCACTTTGTCTACAGCGGTTCTTGAAACAGCGCCACGCACT	5232
OY	4481	GCAAGTCTGTGTCGGGAAACCCCGCTATGGCAAGAGCTGGGACAGTACTTCTCGGTGGGG	4540
Db	5233	GCAAGTCTGTGTCGGGAAACCCCGCTATGGCAAGAGCTGGGACAGTACTTCTCGGTGGGG	5292
OY	4541	CCATGTCGCGCTTCGAAATGCAACTCGGCTATGCCCCAGAGGTCGACAGATTCAGT	4600
Db	5293	CCATGTCGCGCTTCGAAATGCAACTCGGCTATGCCCCAGAGGTCGACAGATTCAGT	5352
OY	4601	GCTTCCTCTGTGCTGGGGCTTTGGCCCAATGGAATGTCTACGCGCCACGTGTGTGTGC	4660
Db	5353	GCTTCCTCTGTGCTGGGGCTTTGGCCCAATGGAATGTCTACGCGCCACGTGTGTGTGC	5412
OY	4661	CGTGTGAGGCACTTCAACAGAGCGCAGGGGCACTCTGTCCCCCTTCCCAAGAC	4720
Db	5413	CGTGTGAGGCACTTCAACAGAGCGCAGGGGCACTCTGTCCCCCTTCCCAAGAC	5472
OY	4721	CGTACTCAACAGGCTCAACTGTGTGTGGAAAGTGTGTGTCCCCGAAAGGCGCTGGCAATCC	4780
Db	5473	CGTACTCAACAGGCTCAACTGTGTGTGGAAAGTGTGTGTCCCCGAAAGGCGCTGGCAATCC	5532
OY	4781	AGATCCAAAGTTGTCAAGTTTGTGAACAGAGCAAGCTGCGTGGAAATATTTGATG	4840
Db	5533	AGATCCAAAGTTGTCAAGTTTGTGAACAGAGCAAGCTGCGTGGAAATATTTGATG	5592
OY	4841	GTGCAATACCTGTAAACCATGCTGGGAGTTTCTACAGAAACAACGTCCTGCTTC	4900
Db	5593	GTGCAATACCTGTAAACCATGCTGGGAGTTTCTACAGAAACAACGTCCTGCTTC	5652
OY	4901	TGAACAGCACTTCCCAACAGGCTCTACCTTCAATTTCTACAGATATCAGGCAATCTGAG	4960
Db	5653	TGAACAGCACTTCCCAACAGGCTCTACCTTCAATTTCTACAGATATCAGGCAATCTGAG	5712

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Db	5713	CTGGCTTC	CACTTG	AGATP	CAAAACGG	TGGGCC	CTGAC	AGTTGG	CCGAAA	CTGTGTG	5772
QY	5021	CCAGTAA	CGGGGT	GAAC	ACTGG	CGAGG	CTACTT	GTGAA	TGATGT	GTCTTCCAGT	5080
Db	5773	CCAGTAA	CGGGGT	GAAC	ACTGG	CGAGG	CTACTT	GTGAA	TGATGT	GTCTTCCAGT	5832
QY	5081	GTGAGC	CGGGAT	TATG	CCCTC	CAAGGG	CCACG	CCACAT	CTCTG	CATGCCC	5140
Db	5833	GTGAGC	CGGGAT	TATG	CCCTC	CAAGGG	CCACG	CCACAT	CTCTG	CATGCCC	5892
QY	5141	GGCGAT	TGGA	ATAC	CCCTC	CTCCAT	CTGTAT	ATGCA	CACTGT	GGGGGAA	5200
Db	5893	GGCGAT	TGGA	ATAC	CCCTC	CTCCAT	CTGTAT	ATGCA	CACTGT	GGGGGAA	5952
QY	5201	TGAG	GGGGGT	GATC	CTTG	AGCCCC	CGGCTT	CCAGG	CACTAC	CCCA	5260
Db	5953	TGAG	GGGGGT	GATC	CTTG	AGCCCC	CGGCTT	CCAGG	CACTAC	CCCA	6012
QY	5261	CCTG	AAAAAT	GAC	ACTG	CCCGT	GGGCTT	TGGAG	CTCA	CATC	5320
Db	6013	CCTG	AAAAAT	GAC	ACTG	CCCGT	GGGCTT	TGGAG	CTCA	CATC	6072
QY	5321	CCGAGC	CCCA	ACCA	GAGT	CACTA	TA	TA	AAATCC	GGAAATG	5380
Db	6073	CCGAGC	CCCA	ACCA	GAGT	CACTA	TA	TA	AAATCC	GGAAATG	6132
QY	5381	TGGG	AGATT	AGT	GGAAG	CGAGG	CTTCC	AAAGCT	CCCTCT	CTCCAG	5440
Db	6133	TGGG	AGATT	AGT	GGAAG	CGAGG	CTTCC	AAAGCT	CCCTCT	CTCCAG	6192
QY	5441	CCGT	GATAT	TTT	CAC	AGCGA	CCACT	CCCA	GAAATCG	GGCAATTC	5499
Db	6193	CCGT	GATAT	TTT	CAC	AGCGA	CCACT	CCCA	GAAATCG	GGCAATTC	6252
QY	5500	-----	-----	-----	-----	-----	-----	-----	-----	-----	5499
Db	6253	ATTG	ACTT	ACT	CCCA	CCAGAT	TTTCT	CTTCT	GAGAG	TTTGT	6312
QY	5500	-----	-----	-----	-----	-----	-----	-----	-----	-----	5499
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QY	5500	-----	-----	-----	-----	-----	-----	-----	-----	-----	5554
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QY	5555	GGGA	GCTG	GGT	CA	AGTGG	GA	CAAT	CA	TG	5614
Db	6433	GGGA	GCTG	GGT	CA	AGTGG	GA	CAAT	CA	TG	6492
QY	5615	TGA	CTGG	GCA	CCCTG	CTC	CA	CGTGT	AA	CA	5674
Db	6493	TGA	CTGG	GCA	CCCTG	CTC	CA	CGTGT	AA	CA	6552
QY	5675	TGCC	CAAT	GTGA	AGTCC	CTTGT	GGCG	GGAA	CA	TACT	5734
Db	6553	TGCC	CAAT	GTGA	AGTCC	CTTGT	GGCG	GGAA	CA	TACT	6612
QY	5735	CCCC	GGGG	TTT	CC	TAG	CCCG	TA	CTT	CCAG	5794
Db	6613	CCCC	GGGG	TTT	CC	TAG	CCCG	TA	CTT	CCAG	6672
QY	5795	CCAT	TGG	GCA	TGG	CGT	CCG	CTC	TA	ACCT	5854
Db	6733	CCAT	TGG	GCA	TGG	CGT	CCG	CTC	TA	ACCT	6732
QY	5855	TCAT	CA	CCAT	CT	GGGA	TGG	AGC	CA	AGAA	5914
Db	6733	TCAT	CA	CCAT	CT	GGGA	TGG	AGC	CA	AGAA	6792
QY	5915	GCAT	GGC	CA	AGAA	CA	AGT	GA	TTT	AT	5974

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 Db 6853 ATGCAAGCCACAGGGGGGATCTTGGCAATAGCTTTCCTGCTTATCCACTCAACCAATGCC 6912
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 Db 6913 CTCCTCCACCAATCTCTCCCAAGCGCGAAGTGGTCAAGAGATGAAGAAATTCATATAG 6972
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DB 10510 CCACCAAG 10546

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LOCUS 8010 bp DNA linear PAT 29-MAR-2003
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1
Alisbrook II, J.P., Anderson, D.W., Burgess, C.E., Boidog, F.L.,
Casman, S.J., Colman, S.D., Edinger, S.R., Eilerman, K., Gerlach, V.,
Gorman, L., Grose, W.M., Guo, X., Hermann, J.L., Kexuda, R.,
Lepley, D.M., Li, L., Macdougall, J.R., Millet, I., Pena, C.E.,

QY	4141	CAGTATGTGGTTCGGACGGAGTGTCTTGTCCCTCCCACTACCCCGAATCAACAGT	4200
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QY	4201	GGACAGATCTGCTTGTATTTTGTACTGTGGCCCAAGAAATATGTGTGTTGGCCAGTTC	4260
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QY	4261	GCCTTCTTTCACACGGGCCCTCAACGACGTGTGGAGTTCAAGAGGCCACAGCCAGAC	4320
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QY	4321	TCCGGGCTCCTCAGCTCCCTTCGGGCTCCCATACAGAGAAATCACTGCTTGGCAAC	4380
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QY	4441	TTTGTCTACCAAGCCGTTCTCTGAAACAGCGCCACAGTCAGTCAAGTCTGTGCCGAACC	4500
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QY	4621	TTGGGCCATGGAATGTCTCAGCGGCCACGTGTGTGTGTGCTGTGGAGGCAATTCACA	4680
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VERSION AY017475.1 GI:14787175
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Sun, P.C., Upadurai, R., Schmidt, A.P., Davis, M.E., Quant, E.C.,
Sunwoo, J.B., Gollin, S.M. and Scholnick, S.B.
Transcript map of the Bp23 putative tumor suppressor region
Genomics 75 (1-3), 17-25 (2001)
TITLE JOURNAL MEDLINE PUBMED
11472063
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Sun, P.C., Upadurai, R., Schmidt, A.P., Davis, M.E., Quant, E.C.,
Sunwoo, J.B., Gollin, S.M. and Scholnick, S.B.
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Submitted (09-JAN-2001) Otolaryngology, Washington University
School of Medicine, Box 8115, 517 S. Euclid Ave, Saint Louis, MO
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QY	703	CAGAAATGACTGTACTTGAGATCTGTGCTGACATTTAGCACTTCAGATGACAAAGTCAAGT	762

Db	1803	CAGATGTGGCTTCAACCTGCAAGTCAGATGACAGCATTTGGCTACCAAG-----	1848
QY	763	TCAGTGAAGGAAGTCTCCAAAAGACTTTCTAATGCTGTGAACTTGTGTCTCTGGACAGAG	822
Db	1849	-----GGTTTAAAGCTGTGATAC-----AAGAA	1871
QY	823	ATCGAAGCAGGGCAAGTTGGCGTGAACCTTGGCATTAAGTGTATGAGCCGAGGGAAGGCTTC	882
Db	1872	ATTGAGAAAGGAGAGCTGTGGGGAGCCCTGGCATCCAGACTATGTGAAGACGACATGGCAGC	1931
QY	883	CGGTTTCAACACGGGTGACACCTCAAGTTTGAAGTGCAGACCGGCTTTGAGCTGTGTGGA	942
Db	1932	AGCTTCTTGCAATGAGACACGCTCACTTTGAGTCCAGGCGAGGCTTTGAGCTGTGTGGA	1991
QY	943	CAGAAAGCAATCACATGCAAGCAAAAAGATTAACCAATGATGTGGCTAAGAAAGCAGCTGGCGT	1002
Db	1992	GAGAGAGTGAATTAAGTGGCAAAAACACAGAGTGTGGGCAACAAAGCAAGCTGTGTG	2051
QY	1003	TTTCTCTGCTTCTTCAACTTCAACAGCCCGCTGTGGGCTGTCTGTCTCCCACTAACCA	1062
Db	2052	TTTTCAATGTTCTTCAACTTCAAGCAGCAACCTCTGGAGTCAATCTCTGCGCAAACTATCT	2111
QY	1063	GAGAGCTATGGCAACACCTCCACTGTGTGTGGCTCATCTCGGCGAAGCCGAGAGCCG	1122
Db	2112	GAGAGTATGGCAACACATGAATCTGTGTGTGTGATTAATGTAGACCTGGAGAGCGG	2171
QY	1123	ATCCACCTGGCGCTTCAACGACATTTGAGCTGAGGCTCAAGTTTGAATTTCTGTGATCAAG	1182
Db	2172	ATTCAACCTCATCTTCAAGAGATTTGAGTGTGGAACCTCAAGTTTGAATTTCTGTGCGGTCAAA	2231
QY	1183	GATGGGGCCACCGCGGAGGCGCCGCTGTGGGACCTTCTCAGGAAAACAAGCTTCCCTCC	1242
Db	2232	GATGATGGGATTTCTGACATCAACAGTCTCGGAACTTTCTCTGGCAATGAGGTGCTGCA	2291
QY	1243	TTCATTCACAGCAATGGCGCAAGTGGCCCGCTGTGAGTTCCAGATGACACTCCACAGGG	1302
Db	2292	CAGCTGGCGACAGATGGAACAATGATGAGCGCTGGAGTTTCAAGTGTGATCACTCCACACT	2351
QY	1303	AAGAGGGGCTTCAACATCACTTTTAACCACTTCCGACACAAAGATGACCGGATCTGTGC	1362
Db	2352	GCGAGAGGTTTCAACATCACTATACATATTCACATTTGTGTGAAACGATGCTCCACAGCCTCGGG	2411
QY	1363	GTTCCAGTAAATGGCAAAACGGTTTGGGGAACGCTCCAGCTGGGCAAGCTCATCTCTTC	1422
Db	2412	ATTCTGTGAAATGGAACGGCGGTTTGGAGACAGGTTTCTGCTGGGAATTCAGTGTCTCTTC	2471
QY	1423	CTCTGTGATGAAGGCTTCTTTGGGATCTCAGGGCTCAAGAGACATCACTGTGCTGTGAAG	1482
Db	2472	CACGTGTATGATGGCTTTTGGAAACATCAAGGGTCTTGAATCCATCAAGTGCATCTTCCAA	2531
QY	1483	GAGGGACGCGGTCTGTGGAACAGGCGTGTGTGGGTGAAGTCCCTGTGTGTGTGCAC	1542
Db	2532	GATGGAATGTGGTCTGTGAGCTTCACTGTCTCTGCTGTGAAGTCCATGTGTGTGGGCAAC	2591
QY	1543	CTGACTTTCGCCACGCGCACCATCTCTCTCCGGGCTGGGCTGTGCTTCAAGAGATGCC	1602
Db	2592	CTGACGGGCTTCAGATGGGGGTCAATTAATCTCCAGAGATGGCGGGATATCTAAGAAATTC	2651
QY	1603	TTGAGCTGTGCTGGGTGATTTGAGGCGCCACGACAGCTAACCCCATCAAAATCACTTGCAC	1662
Db	2652	TTAAACGTGTAAATGGGTCAATTTGAAGCAAAAACAGAGACATTCATCAAGATTAACCTTGAC	2711
QY	1663	AGATTCAAAACCGAGGTCAACTATGAAACCTGTGAATTAAGCATATGGGCGGAGCTTACTCA	1722
Db	2712	AGGTTCCAGACAGAGTCAATTTATGATTAAGCTGTGAATTAAGGATGGGAGCCAAACAGCTCA	2771
QY	1723	GGCGCCCTTGAATCGGGGTTTACACAGGAGACCCAGATTCCCAAGTTTCCATCAAGACAGC	1782
Db	2772	TCCCACTCATATGGAAGATACACAGGACCCAGGCAACAAAGTTCTCTCATCAAGACAGGC	2831
QY	1783	AAGTAAGCTTAAGTCTCTCTTCTTACCGCAAGAGATCACTGGACATCGGCTTCCAGCTC	1842
Db	2832	AAGTAAGTAAAGTCTCTGTTTATACATGATGACAGCGGGCTAAGCTTGGCTTCTCATC	2891

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2892 CACTATGAGAGTGTACTCTTGAATCCGACTCTGTCTGACCCAGGACTCCCTGTAAT 2951
1903 GGAACAGCTCATGGAGATGATCTTACGTGGCGCGCTGGTGAACCTTCAGCTGTGACTCG 1962
2952 GGTACAGCCGATGGCAGTAACTTTGGTATCAGGTCTACAGTGAACCTTCAGCTGTGACCT 3011
1963 GGCTACACTTAAGTGAACGGGAGGAGCTCTGGAGTGGAGCCCACTTCAGTGGAGCCGG 2022
3012 GGGTACACACTGAGTACGATAGAGCCCTGTCTGGAGAGAGAACATAGTGAACCAAC 3071
2023 GCCCTGCCAGTTGGAGAACTCTGTGGTGGCTTCAATTCAGAGCTCCAGGAGCAATC 2082
3072 GCTTGGCCAGCTGTGATGCTCTGTGTGGAGGCTACATCAGGAAGAGTGGAGCTGTG 3131
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3132 CTTTCTCCAGGATTTCCAGACTTTTATCCAACTCTGAACTGTACATGAGCAATCGAA 3191
2143 ACATCTCAGGAGAGGGTGTCTTCACTTTCACACTTCACCTGCAAGTGGCCAT 2202
3192 GTCTCTCATGGCAAGGAGTGAAGATGAAATTTCCACACTTCACCTTGAAGTTCCAC 3251
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3552 AAGCTTACTGCTGGGTGGGAGCGCGAGTGTGAGTCACTCTGCAAGTGTGTG 3611
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3852 GTGTCTCAACAGACCTCCAACTACCTGAGGCTGAGTTCAACACCAACGGGTCCGACAC 3911
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Db 7032 AATGAG 7091
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OY	2200	CATGACTACTCTCTCATCTGAGAAACGGACAGTTCACCCAGCCCTGAGGACACTAAT	2259
Db	3334	CACGACTATTTACTGATCTACAGAGGATGGAAAGTTTTTCCAGGCCGTTGCCAGGCTCAC	3393
OY	2260	GGATTCGGCTGCGCAGCTTCCATCAGCGCTGGGCTTATGGCAATTCATCTGCCAGGTC	2319
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OY	2320	CGCTTCATCTCGAATTTCTCCATGTCATATGAAGATTCAACTACACTTCTCAGAGTAC	2379
Db	3454	CGGTTATATACAGACTTCTCAATTTTCGACGAGGCTTCAATACACTTTCAGAATAT	3513
OY	2380	GACTTGAGCCCTGTGAGAGCCCGAGGTCCGAGCTACAGCATCCGAGAGGCTTGGCAG	2439
Db	3514	GACCTGGAGCATGTGATGATCTTGAGATCCCTGGCTTCAGCCGAGAAATGGTTTTCAC	3573
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Db	3574	TTTGGTGTGGGAGACTCTCTGACGTTTTCTGCTTCCGGGATATCGTTTGAAGAGTGC	3633
OY	2500	GCCCCATCACGTGCTGGGGGGGACAGACGGCGCCTGTGGAGCTCGCCTCTGCAAGGTG	2559
Db	3634	ACCAAGCTTACCTGCTGGGTGGGGCCGCCGTGTGTGATGACCTCTGCCAAGGTG	3693
OY	2560	GTTGCTGAGTGTGGGAATTCAGTCAAGGCACTCAGGGTACTTGTGTCCCCCACTT	2619
Db	3694	GTTGGCGAATGTGGGACAGATGTCCAAAGAAATGAAAGAAATTACTGTCTCCAAATTTT	3753
OY	2620	CCTGGAACCTCAATTAACATATGAAATGCAATCTACCTCAGACCCAGCCAGGGAG	2679
Db	3754	CCATCCAAATTATGATATAACCAATGAGTATCTTATAAATGAAACAGAACCGGCAAG	3813
OY	2660	GGAATTCAGCTGAAAACGAGGAGCATTTGMACTCTCCGAGAGAGATGTCTCAAGTTTAT	2739
Db	3814	GGCATCCACCTTAGAACACAGAAAGCTTCAGCTGTTTGAAGAGATATCTTAAAGGTATAT	3873
OY	2740	GATGGCAACACACTCCGCCCGCTTGTCTGGAGATTTTAAACCATCTGAAATGATGGG	2799
Db	3874	GATGGAAAAGACAGTTTCTCAAGTCCATCTGGGACGTTCACTAATAAAGAACTTCTGGG	3933
OY	2800	GTCATTTGGAACAGCAACATCCAGCAGTCTGTGGCTTGATTTCACTACATGATCTGAAAC	2859
Db	3934	CTGATCTCAAAACGACATCCAACTCACTGTGGCTGAGTTCAACACCAATGATCTGAC	3993
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Db	3994	ACCGACCAAGGTTTTCACATCACTCACTATCCAGTTTGTATCTGTAATAATGAGAGATCCG	4053
OY	2920	GGAAACCCCAAGTTTGGCTCAAGGTTATATATGAAGTCAATTTTGCAGGGAGCTCCGTG	2979
Db	4054	GGCATCTCTTAATAGCGGCTATATAGATCCGTATGAGGCCACTTATCCGACATCTGTAATT	4113
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OY	3040	GGAGAGCCCGGACCTGGGACCGGCTTCTGCCACCTGTGTGCGCGAGTGTGGAGGACA	3099
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Db	4414	AGTGAATCTCTGTGAAGAGATGGAGTGGTCTCGCCCTTCCGGAGGACATTCACAGCAC	4473
OY	3340	TTCAACTGGGTGCTCTGCTGACGTTGACACTGACTTTTTCACACAGCAAGAGGGCTTTGGC	3399
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OY	3580	CAGCCACGCCCCCAACATGATGAGTCTCTCGCGGGGAGACTCTGACAGAACATCTTGG	3639
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OY	3700	GTGACCGTCTCAGCAGACTACGTCATGCGCCCTGTGATTTAACATCTTTAACTTGAAGCT	3759
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OY	3820	TTCTATGGCTCCAGCTCCCGAGGCGGCAATGAAGCAGCGACAGCTCTTCTGGCC	3879
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OY	3940	CGGAGTCATGTTTGTGATCTGTGTTTCAATCAAGAACGGCACAGGGGTGGGCTCCGACTG	3999
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Db	5134	AAGCTGGCTCCACCATTCACCTACAGTGTGACTGTGGCTATTAAGATTCTTGAACCCCTCA	5193
OY	4060	AACCTGACTGCATCTGTGGGCTGTGATGGAGAGCCGTTGTGAACAATATCCCGGCGCACTG	4119
Db	5194	TCCATCACTGTGTGATTTGGGGCTGATGGGAAACCTCTGTGGACCAAGTCTGCTCC	5253
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OY	4240	TATGTGGTGTGGCAGGTGTGGCTCTTTTACACAGGCGCTCAACGACGTGTGGAGGTT	4299
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Qy	5737	CCGGGGTTCCTTAGCCGTACTCAAGCTCCAGAGCTGTGTCTGGCTGATCAACCGTCCG	5796
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Qy	6157	TGCAAACTTGGAAACCTACCTGACAGTTTGAAGAACACCCCGCATATATGAAATGCACTGT	6216
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 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

REFERENCE 1
 AUTHORS Weicher, A.A. and Elliott, G.S.
 TITLE C3b/iC3b complement receptor-like molecules and uses thereof
 JOURNAL Patent: WO 0210199-A 3 07-FEB-2002;
 Amgen Inc. (US)

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ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1 WeiJcher,A.A. and Elliott,G.S.		
JOURNAL	C3b/c4b complement receptor-like molecules and uses thereof		
	Patent: WO 0210199-A 6 07-FEB-2002;		

Angen Inc. (US)

FEATURES

source

CDS

Location/Qualifiers

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Query Match 40.1%; Score 4067.4; DB 6; Length 10433;

Best Local Similarity 65.5%; Pred. No. 0;

Matches 6001, Conservative 5, Mismatches 3136; Indels 25; Gaps 3;

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OY	7659	ACACCAAGAAAATAGTGTTCGTCAAGGTCCACGCGCGGCGCC	GGACAGGTTCAAGTTCCG	7718
Db	7008	CTTTGTGGAAAATGCAATTCGTACAGGGCAACAGACTTTCTT	GTAGATGG	7067
OY	7719	CACCACTGTGTCTTAACCGGTGCACACAGGCTTCTACTCT	GTGGCAACCCAGTGTCA	7778
Db	7068	AATAGTATTCCTGTACATGTGAAGAGATTTACTTGTCTGG	ATCTTCAGCTTGAC	7127
OY	7779	CTGCCAGGGAATGGCAATGGAACTTCGCCCCCGCCAGATGT	CTCTTGGTCTGTGG	7838
Db	7128	CTGTATGGCAATGGCTTATGTGGACCGATCCCTGCCAAAG	TTTGGCTAATGTGTGG	7187
OY	7839	CCATCCGGAGCTCCCGGCTCACTCCCAATGTCTGGAGACAG	TATATCTGTGGAGCAGT	7898
Db	7188	ACACCCAGGGGTCCCTGCAACGCGCTCTCACTGGAGAGCT	GTTTACTATATGGCGCGT	7247
OY	7899	GGTGGGTATACAGCTGACATCGGCAGACGTACTCTGGTGG	AAACAGCAACCCGATGTGG	7958
Db	7248	CGTGCACTACTCTGACAGAGGAGAGAGCTCATATAGCA	ACGACAGATGTGGCA	7307
OY	7959	GCTGGATGACATCTGACCTGGCTCCCTCCCTCACTGCT	CAAGAACAGCGTGGAGTTTG	8018
Db	7308	GGAAACACAGTCACTGGAGCGGGGCACTGCCCACTGCA	CACAGAAATATCTGTGATCTGT	7367
OY	8019	CGGTGACCTGGGATCCCGGCTCATATGGGATCCGTTTGG	GGGACAGCTTTGATCCAGGAC	8078
Db	7368	TGTGTATCCGGGAGCCCAAGCAATGGGTCGTGGCTGTG	ATGATCACTTTAAGACAAAGAG	7427
OY	8079	TGTATGCGCTTCAAGCTGTGAAGCTGGCCACAGTGTCT	CCGGGATCTGTACAGCGCACCTG	8138
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OY	8499	CAAGGACCGGACATGAAATGGAACCAAGCCCGTCTG	CAAGACTCTCATGTGCAACCAAC	8558

Db	7848	CAAGAGCGCAGTGGAAATCCGACGAAACCTGTCTGCAAGCCGCTGCTGTCTCTCAACC	7907
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AUTHORS	Welcher, A. A. and Elliott, G. S.	
TITLE	C3b/c4b complement receptor-1-like molecules and uses thereof	
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Query Match	Best Local Similarity	Matches 6001: Conservative	Score 4067.4;	DB 6;	Length 10673;
	65.5%;	5; Mismatches 3136;	Pred. No. 0;	Indels 25;	Gaps 3;
QY	819	AGAGATGAGCAGGGCAGTTGCGGTGA	CCCTGCGATACCTGATATGCGCGGAGGAAAG	878	
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QY	879	CTCCCGGTTTCAACAGGTGACACACTCAAGTTTGAAGTGGCAGCGCGCTTTGAGCTGGT	938		
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QY	999	CGTGTCTCTGCTTTTCAACTTACACAGCGCCCTTGGGGTGTGCTGTGTCCCACTA	1058		
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QY	1059	CCGAGAGCATATGGCAACCACTTCCACTGTGTCTGGCTCATCTGTGGCAGAGCTGAGAG	1118		
DB	648	TTCAGAGGAATATGGGAACAATGAACTGTGTCTGTATTAATCTCGAGCCAGAGAG	707		
QY	1119	CCGATATCCCTGGCTTTCAACGACATTTAGCTGGAAGCTTCAAGTTTGAATTTCTGTGTAT	1178		
DB	708	TGCAATTCACCTTAATCTTTATATGATTTTGAATGTTGAGGCTCAATTTTGACTTTTCCGCGGT	767		
QY	1179	CAAGATGGGGCCACCGCGCAGAGGGCGCCGTCTGGGACCTTTCAGAGAAACAGCTTCC	1238		
DB	768	CAAGGATATGACATTTTGAACATTAATCTGTCTGGGATCTTTTCTGGCAATGAAGTCC	827		
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Qy	5859	CACCATCTGGAGTGGGGCCACAGCAAAAGCACAGGGCTGGGCGTCTCACCCGGAGAT	5918
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Db	5508	AGCCCTCGAAAGGGGTATAGTCTCACCAACCAACTCTGTCTCAAGTTTCCACAGGACT	5566
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Qy	6039	TCCCAACATCCCTCCCAACGCGGAAGTGGTCAAGAGATGAAGAAATTCATATATGGGA	6098
Db	5628	TCCCCAGCGGTTCCACAGGCAAGAAATGCTTACTAGATATGATGATTTTCAGATATGGGA	5687
Qy	6099	CATCGTACGCTACAGATGCTCCCTGGCTTTTACCTTAGTGGGGAATGAATTTCTGACCTG	6158
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Qy	6159	CAAACTTGGAACTTACCTGAGTTTGAAGACCAACCCCGATATGTGAAGTGCACTGTC	6218
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Qy	6219	AACAATAGCTTTCAGACGATCCACAGGCGTATCTGAGCCAGACTACCTTGGAG	6278
Db	5808	AGCAATGAAGTCGGAGCTGATCATCGGAATCATTTCACTCAGTCCAGGGTATCCGGATGA	5867
Qy	6279	CTATCCCAAGTTCCAGACCTGCTCTTGGCTGGTGAAGTGAAGCCGACTTAACTATTC	6338
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Qy	6339	TCATACAGACAGAGTCTCTGTGCTGAAGCCCTCAGTGGGAATTACTAGCTCCCCGTAT	6458
Db	5988	TTCTTCTGGGCAAACTCCTGTGCTATGATGTTAAGTGGGAATCATACGAACATCAAA	6047
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Qy	6519	GAAAGGCTTCAGATCCGCTATTACGCCCTTACTGCAAGCCTGCGCCAGAGGCTCCACTCA	6578
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KEYWORDS
SOURCE Homo sapiens (human)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE 1
AUTHORS Shinkler, R.A., Lichenstein, H., Vernet, C. and Fernandez, E.
TITLE Polypeptides and nucleic acids encoding same
JOURNAL Patent: WO 013663-A 31 25-MAY-2001;
Curagen Corporation (US)
FEATURES
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REFERENCE
 1 Shinkels, R.A., Lichenstein, H., Vernet, C. and Fernandes, F.
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 Patent: WO 0136638-A 29 25-MAY-2001;
 Curagen Corporation (US)

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ORGANISM	Homo sapiens

REFERENCE
AUTHORS

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Tanigami, A., Fujiwara, T., Shibahara, T., Goto, Y., Hirao, M.,
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TITLE
NEDO human cDNA sequencing project
Shimizu, F., Wakebe, H., Ono, T., Hishigaki, H., Matenabe, T., Ozeki, K., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakematsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai, Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yanaashita, H., Matsumo, K., Nakamura, Y., Sekine, M., Takachi, H., Kande, K., Wagatsuma, M., Murakawa, K., Kanehori, K., Kikuchi, Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahori, K., Masuno, Y., Nagai, K. and Isega, T.

JOURNAL REFERENCE AUTHORS TITLE JOURNAL	COMMENT
Unpublished 2 (bases 1 to 4380) Isogai, T. and Yamamoto, J. Direct Submission	
Submitted (15-JUL-2003) Takao Isogai, FLJ Project (HRI Team); 2-6-7 Kazusa-Kamatari, Katsurazu, Chiba 232-0818, Japan (E-mail:genom@eshrf.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)	NEO human cDNA sequencing project supported by Ministry of

Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB) / cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5' & 3' end on pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: Reverse Proteomics Research Institute, HRI and RAB.

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REFERENCE
 AUTHORS
 TITLE
 1 Shimizu, A., Asakawa, S., Sasaki, T., Yamazaki, S., Yamagata, H., Kudoh, J., Minoshima, S., Kondo, I. and Shimizu, N.
 A novel giant gene CSMD3 encoding a protein with CUB and sushi multiple domains: a candidate gene for benign adult familial myoclonic epilepsy on human chromosome 8q23.3-q24.1
 JOURNAL
 Biochem. Biophys. Res. Commun. 309 (1), 143-154 (2003)
 MEDLINE
 22824680
 PUBMED
 12943675

REFERENCE

2 (bases 1 to 13040)
 Shimizu, N., Asakawa, S. and Shimizu, A.
 Direct Submission
 Submitted (11-JUL-2003) Nobuyoshi Shimizu, Keio University School
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 160-8582, Japan (E-mail: nshimizu@med.keio.ac.jp).
 Tel:81-3-3351-2370, Fax:81-3-3351-2370

FEATURES

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Location/Qualifiers

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ORIGIN

Query Match 33.9%; Score 3435.6; DB 9; Length 13040;
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 QY 9281 CACTGCCGGGAGCCACCGCTCAACCAAGCTTGAATCTGTGGGATGTTTGGCAAGAA 9340
 DB 10485 ACTTGCACTGGAAACCCAGCCCAAGCTTAAGTGTCTGTATGTATTTGGCCAAA 10544
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 DB 10545 TTAATATGGAAGAGGCTTTCAATTTCAAGGAAGGAACAACCATGACCTTAACAT 10604
 QY 9401 GACTGCTTCAAGTTGCCAAGCAGAGTCAATGTCCACATGATGACACACAGTGGCGT 9460
 DB 10605 TACTATTTCAATGTCTTCCACTGGAGATTAACGMACTGCA--GCMAATAGCAACAT 10661
 QY 9461 GGAAGTCACTTGGCTGGAACCTTACAAAGAAAGATTTTCAATCTCTCACTCCAGGTGA 9520
 DB 10662 GAGCTGCTACTTTCAAGGGGTATATTAAGCCAGAAAGTCCGCTATATTTAGCATATTA 10721
 QY 9521 CCAAGTTACAGGCTGTGAGAGATCTTATGATTAAGTTCAAGATGATCACTGGCTTT 9580
 DB 10722 TCTTATTAAGTACGCTCATGCTTCTGTGAAGAAATGGAAGAAATTTGGCAAT 10781
 QY 9581 AGATGGCAATGTCTGTGATGAGTCTCCGAGCACCTTCACTATCAAGGCTCTGTCA 9640
 DB 10782 GGAATGCTTGTGTTGCTGAGACCTGATGAGTACTTATGTATTTCAAGGAATTTATTA 10841
 QY 9641 GGGCCAAAGCTTTGGGCAATGTGGCTTTCAAAAGATGAGACTCAGGCTGTGAGTCA 9700

Db 1560 CAGCAAGATTCTTCTAATGAGGAGGATTAAAAACAGTTCCTCCATTATGCC 1619
Qy 225 AGACCTGGCATACCCGAAAGGGCAAAAGACTAGCTCGGATTTGAGTTAGATCCAG 284
Db 1620 AGATCCAGAGAAACGAAATGGAAGAGATCGATCATGATTTTAGCTTGATCAAC 1679
Qy 285 CGTCCAGTTTCACTGCAAGAGGGCTATGACTGCAAGGGTCCAAAGGATCACTGTAT 344
Db 1680 TGTGCAAGTTCTCTTGTGATGAAATATATGCTTACAGGGGGCAAAAGATCAGTCTCA 1739
Qy 345 GAAAGTAGCGACATTTTGGGCTCGAGCGAACCAAGCGAGTCTGCCAGCCGCAT 404
Db 1740 ACGGATAGCTGAAGTTTGTCTGCTGAGTATCAAGGCTGTGTGTAAGTAAAC 1799
Qy 405 GTGTGATGCCACCTTTCAGAGCCCTCGGATCATCACTCCGCCAATTTCCCATTTCA 464
Db 1800 GTGTGCTCTTAATCTTCAAGGACCAAGTGTATCTTTACATCTCCAACTTTCCTTCA 1859
Qy 465 GTATGACAAATGACACACTGTGTGATCATCAGACACTCAACCCCTCCAAAGGTGAT 524
Db 1860 GTATGACAGCAATGACATATGTCTGTGGTATCAGACAGTGAATACAAATTAAGTTAT 1919
Qy 525 CAAGCTCGCTTTGAGAGTTGATTTGAGAGAGGGCTATGACACCTGACGGTGGTGA 584
Db 1920 CCAGATTAATTTTGAAGAAATTTGATCTGAGATTGGCTATGATACCTTGAATTTGGCGA 1979
Qy 585 TGTGTGTACAGATGGGGACCAAGAACATTTCTCTACATGTCTCAAAATGCTCGACGTGA 644
Db 1980 TGGGGGCGAAGTTGGAGATCTTAGACAGTGTCCAAAGT- 2019
Qy 645 CAGCCTTCAACCCGAGGCTCTGCAATCCAGAGACATGTGGGGAACATCGAGGCA 704
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Qy 705 GAAATGAGCTGTACTTGAGATCTGTCTGTGACATTTAGCAAGTTAGATGCAAGTTCAGGTTTC 764
Db 2079 CTTTCAACGAGAG- 2092
Qy 765 AGTGAAGAAAGTCTCCAAAGCTTCTAATGCTGTGGAACCTTGTCTCTGGACAGAGAT 824
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Qy 825 CGAGCAGGAGATTTGGGTGACCTCTGACATCTGATATGAGCGGAGGAGGAGCTCCG 884
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Qy 885 GTTTCACACGAGTACACACTCAAGTTTGAAGTCCAGCCGCTTTGAGCTGTGGAGCA 944
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Qy 945 GAAGGCAATCATGCTCCAAAGAAATTAACATGTGTGGCTAGAGAGCCAGGCTGCTGTT 1004
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Qy 1065 GGAATATGGAACCACTTCATCTGTGTCTGCTCATCTGAGCCAGGCTGAGAGCCGAT 1124
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Qy 1125 CCACTGAGCTTAAAGCAATTAAGAGTGTGAGCTCAGTTTGAATTTCTGTGATCAAGGA 1184
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Qy 1185 TGGGGCAGCGAGGAGCGCGCTCTGAGGACCTTCTGAGAAACAGAGTCTCCCTCCTC 1244
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Qy 1245 CATCAAGACAGTGGCAGTGGCCGCTCTGAGTTCAAGACTGACCACTCCACAGGGA 1304
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Qy 1305 GAGGGCTTCAACATCACTTTTACACCTTCCGACACAGAGTCCCGGATCTGGCGT 1364
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Qy 1365 TCCAGTAATGGAACAGGTTTGGGACAGCTCCAGCTGGGAGGCTCCATCTCTTCT 1424
Db 2676 ACCAATCATGACCGCGGTTTGGGGAACAATTGAAATTAAGAAATTAATTAAGTTAT 2735
Qy 1425 CTGTGTAAGGCTTCTTGGGACTGAGGCTCAGACCAATCACTGCTCTGAAGGA 1484
Db 2736 TTGTGAAGAGGATTTATTAACCCAGGGAACAGAAACAAATTAATTAATTTATGA 2795
Qy 1485 GGGCAGCGTGTCTGGAACAGGCTGTGTGGGTGTGAAGCTCCCTGTGTGTACCT 1544
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Qy 1605 GAGCTGTCTGTGTGATGAGGCCAGGCTAACCCATCAAAATCACTTGCAGAG 1664
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Qy 1725 GCCCTGATCGGGGTTTACACAGGAGCCAGGTTCCCAAGTTCTCTATCAGACACAGAA 1784
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Qy 1905 ACAGGCTATGGAATGAATCTTACGTGGGCGCTGTGATGACCTTACGTGATCGG 1964
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Qy 1965 CTACATTAATGAGAGGAGCTCTGAGTGTGAGCCAACTTCAAGTGAAGCCGAGC 2024
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Qy 2085 GTGCGAGGTTCCCTGACTTACCCCAACAACTTGAACCTGATTAATGGAAC 2144
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 QY 2445 CGTGGGCGGACACTTGGACCTTCTCCCTGCTCCCGGGATACGGTGTGAGAGGACCGGCCG 2504
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 QY 3105 AGGAGAGTGTGCGGGCAGGTGCTGTACCCGGGTATCCAGCTCCCTATGAACACATCT 3164
 DB 4416 AGGAGATCATTCAGAAAGATCTTATCTCTGTCTATCTTTTCCATATGACATTAACCT 4475
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 Qy 6705 GTGAGCGAAGCATCTCTGTCTCAAGCTTTTCTGTGGGCTTCTGAGGCCCCCA 6764
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QY	6765	GAATGGAATGGTGTGTTGGCAAGAGATACACAGTGGGAACCAAGGCCGTGTAACAGTGCAG	6824
Db	8076	AAATGGAGAAATACTAAACACAGCATTAATTTGGTAGAAACGGGAATTACATATTTTGTAA	8135
QY	6825	TGAAGGCTACACACCTCCAGGAGGCGCTGAGGGCCACTGACAGAGTGTGACACAGGCT	6884
Db	8136	TGATGGATATGATGTTGATTCATCCAAAGAACTCACTACAGCTGTATGCCAATCAAGTGGAA	8195
QY	6885	ATGAGCAACCGCAATGTCCACCACAAGTGTGCTCTGTGACTTGTCTGATGTCAATG	6944
Db	8196	ATGGAGCAATCATTAACAGAACCCCTCGCTGTGTTGTGTATCATGTCCAAAGCATCAATTC	8255
QY	6945	CATCAGCCTGGAGCATGGCCGATGAGGCTTATCTTTGAGACAAAGATATCAAGTTCCAGC	7004
Db	8256	CTTATATCTTGGAACATGGAAATGGCGAATTTGTAAATGGCTCCCATTAATGAATCAAAAC	8315
QY	7005	CCAGCTATGCTCATCTGTGACCCCTGGGCTACTCATATCTGGCCAAAGGGCATCCGCTG	7064
Db	8316	CAAACTAGTTTCACTGTGACCTCGGTTATCATGACTAGGTCTGCTCCATCGAATG	8375
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 REFERENCE 1 (bases 1 to 10944)
 Sunwoo, J.B., Gollin, S.M., and Scholnick, S.B.
 Transcription map of the 8p23 putative tumor suppressor region
 Genomics 75 (1-3), 17-25 (2001)
 JOURNAL 21365705
 MEDLINE 11472063
 PUBMED 2 (bases 1 to 10944)
 REFERENCES
 Sun, P.C., Uppaluri, R., Schmidt, A.P., Davis, M.E., Quant, E.C.,
 Sunwoo, J.B., Gollin, S.M., and Scholnick, S.B.
 Direct Submision
 Submitted (08-JAN-2001) Otolaryngology, Washington University
 School of Medicine, Box 8115, 517 S. Euclid Ave, Saint Louis, MO
 63110, USA
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ORIGIN

Query Match 33.4%; Score 3387.8; DB 9; Length 10944;
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Db      9940 CCATGAGCTGAAGTTGACAGGCAATTAACAAGAGAGAGGCCCACTTACTCTGAAA 9999
Qy      9516 GTGTACAGATTTACAGGCGCTGTGAGATCTTTATGATAAGTTCAAGATGATCACTGG 9575
Db      10000 GCTTTTAAATTAAGGCGCAGGCGAGATATTTTGTAAAGCAAGTTGAAATGACACTGG 10059
Qy      9576 GCTTTAGATGGCCATGTCTGTGAGAGTCTCCGAGCCACCTTCATCTACCAAGGCTCT 9635
Db      10060 GGACTGATGATGTATGTGTATGCTATGAGCTTGAAGAGAGGATTTACTTTCAAGGTGAC 10119
Qy      9636 GTCAAGGCGCAAGCTTTGGGAGTGTGGCTTTCAAGACTGCACTCAGGCTCTGAG 9695
Db      10120 ATTCATGGAAGAAAGCTTTGGAAATTTAAGCTAGAAAGGCAAG-----TCTTTTAAAC 10173
Qy      9696 TCAAGCCCGAGTCAATTTGGCCGCACTTTGTCTTCAACAGCAGCTCAGTGGAGCCGCG 9755
Db      10174 CCAGATCAAGACTTTCAGTCAATTAACAGGACACAGCAGAGTGTCTGTGGGCTGCC 10233
Qy      9756 ATCTGTGCTTTTCATGCGCCCTCATTAATTTGGGGCTTGTGTCTTATCTTCAAGCAC 9815
Db      10234 ATTTGTGCTTTCTTTTGTCTTATTTTATCAGGGTTTGATTTTACCTTACAAACAC 10293
Qy      9816 AGGAGAAAGCCAAAGTTCTTTCAATGTGCTATGTGCGCCACGAAACCAATGTTGG 9875
Db      10294 AGAAGAGACCAAAAGTTCAATCAATGCTATGCTGGGCTATGAAACAGCAATGACAA 10353
Qy      9876 GCCCATTTTGAAGCCCAATGTATGACCGCAACATTCACAGCCCAAGATGAGCCAGC 9935
Db      10354 GCATGTTTGAAGCCCATGTATGATACAACTTTAAACCAAGAGAGCAGAGGCTGTG 10413
Qy      9936 GAGCGAGGTTCAAGTACAGCAGTGTGACAGCAGTATAGCCAGC 9984
Db      10414 AGTTTGAACAACCTGGAACAGAGTGTATGAGTGTGCTGAG 10462

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Search completed: October 19, 2004, 09:50:16
Job time : 27655 secs


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Db      8382 ACACATACCTGAGCAGCTTGTACTATAGTGTGACCCCGGATATGTGTGAATGGCACTG 8441
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Db      8442 AGAGGAAATGCTCCAGATGACAAAACCTGGATAGATGAGGCCATTTGTGATTCCTG 8501
QY      7466 TTACTGTGGACACCCAGGCAACCTGTCAACGGCTCACTCAGGTTAACAGTTTAACC 7525
Db      8502 TGGACGTGAGTTACCCCGCAGTCTCAGCCATATGGCCAGGTGAGAGACAGATACACT 8561
QY      7526 TCACCATGTGTCAAGTTTGTGTGCAACCTGGGTATATGTGTAGGGGGCTGTAGGT 7585
Db      8562 TCCAAAAGATTTGAATACCTTGCAATGAGGGTTCTGTGTAGGAGCCAGGAGTC 8621
QY      7586 CCCAATGCTGGCCAGGGGCAATGAGTGTGACATGTGCCCACCTGCAATATCAATCACT 7645
Db      8622 GGGTTGTCTTGTCCAAATGGAATTTGAGTGTGAGCCACTCCGACTGTGTGCTGTCAAGT 8681
QY      7646 GTACAGATCTGTGACACCAAGAAATATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 7705
Db      8682 GTGCCACCCCGCCACAACTGGCCAAATGGGGTGTGCGGAAGGCTGTGACTATGGC----- 8734
QY      7706 GGTTCAGCTTGGCACCACCTGTGTCTTACCGGTGTGCAACAGGCTTTTCACTCTGTGGCA 7765
Db      8735 -----TTCAATGAAGAAATGTAACATTCACATGTATGAGGGCTAATCTTGTGACGGTG 8786
QY      7766 CCCCATGTCTAGCTGCTGCCAGGGAGATGGCAATGGGACCGTCCCGCCCGCCAGTGTCT 7825
Db      8787 CTCCAAAATCTACCTTCTCATGTGATGAGGCACTGGGATGCAAGATTTCTCTGTAAAC 8846
QY      7826 TGGTGTCTGTGTGGCCATCCGGGCTCCCGCTCACTCCAGATGTGTGAGACAGTTATA 7885
Db      8847 CAGTCAACTGTGTGACCTCTCTGAAGATCTTGGCCATGTTTCCCTAATGTTTCTCTTTA 8906
QY      7886 CTGTGGGACATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 7945
Db      8907 TTTATGTGGGCAATATACATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 8966
QY      7946 CCCCATGTGTGGGCTGTATGTGACATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 8005
Db      8967 CAAGAAAGT-----GCTCTCCAAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 9014
QY      8006 GCGTGGGATTTGCGGTGACCTGTGGATCCGGCTCATATGGCATCCGTTTGGGGGACAGT 8065
Db      9015 GCGTGCCTTGACAGATGTTCACACACAGTATATGAAATATGAACTGTCAATGGACAGATT 9074
QY      8066 TTGATCCAGGCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 8125
Db      9075 TTGACTGTGTGAAGGAGCGGATTCAGTGTCTTCAAGGCTTCAAGGCTTCAAGGACTTT 9134
QY      8126 CAGAGCGCACCTGTCAAGGCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 8185
Db      9135 CTGAATATCACTGTGTGAAGGCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 9194
QY      8186 TCTCTTTTGGGAACCTGTGGGACTCCAAGTATGC 8219
Db      9195 CTTCTGTGTGTGTCTCTTCCAATGATACCAATATGC 9228

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RESULT 2
US-09-911-842A-3
Sequence 3, Application US/0911842A
Patent No. 6656707
GENERAL INFORMATION:

APPLICANT: Amgen Inc.
TITLE OF INVENTION: C3B/C4B COMPLEMENT RECEPTOR-LIKE MOLECULES AND USES THEREOF
FILE REFERENCE: 0107/37592
CURRENT APPLICATION NUMBER: US/09/911,842A
CURRENT FILING DATE: 2001-07-24
PRIOR APPLICATION NUMBER: US 60/222,438
PRIOR FILING DATE: 2000-08-01
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patent version 3.0

SEQ ID NO 3
LENGTH: 11230
TYPE: DNA
ORGANISM: Mus musculus
US-09-911-842A-3

Query Match 1.0%; Score 100.8; DB 4; Length 11230;
Best Local Similarity 45.6%; Pred. No. 66-17; Indels 15; Gaps 1;
Matches 409; Conservative 0; Mismatches 472;

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QY      7100 GCGCCACCTGCGCATCATCTCTGTGTGAGAGTCTCCGATTTCCGCCAATGAGCCACCGCA 7159
Db      8292 CACCTCTTGTGATTTCAATGATATGATTTGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 8351
QY      7160 TCGGAACACTGTCTGTCTACCGGGCAACAGCATTTCTCTGCAATTCGGATACAC 7219
Db      8352 ATTTCACACACACATATGAGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 8411
QY      7220 TGTGGGCTCCAGGGGTGTGATGTGACATGGCCAAATGGGCTGTGAGTGTGTGTGTGTGTGTGT 7279
Db      8412 TAGAAGGCTCCCACTTAAGACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 8471
QY      7280 GCTGCTTGTGTGACACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 7339
Db      8472 GCTGTGAAGGCATCTCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 8531
QY      7340 AGAATACAGTTACCGGGGCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 7399
Db      8532 ATGACTATCTCTTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 8591
QY      7400 GCATGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 7459
Db      8592 GCTCTAAGAGAGACATGTCCAAATAATGAGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 8651
QY      7460 TGGCAATTACTGTGTGACACCCAGGCAACCTGTGTCAACCGGCTTCACTCAGGTAAACA 7519
Db      8652 TTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 8711
QY      7520 TTAATCTCAAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 7579
Db      8712 ACACATTCCAAAAGAAATTAATCATATCTTGTGCGTGTGAAGGTTTATCTGTGAAGAGCCA 8771
QY      7580 CTAGTGTCCAAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 7639
Db      8772 GGAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 8831
QY      7640 TCAACTGTACAGATCTGTGACACCAAGAAATATGTGTGTGTGTGTGTGTGTGTGTGTGTGT 7699
Db      8832 TTATATGTCTGCGCCACACACAGGTGCCAAATGGGGTGTGAGATGGCTGTAGC----- 8884
QY      7700 CGCACAGTTCAAGTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 7759
Db      8885 -----TATGGTTTCAAGAGAAATGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 8936
QY      7760 TGGGCAACCCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 7819
Db      8937 AGGGGGCTCCAAAGACTACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 8996
QY      7820 GTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 7879
Db      8997 GTAAACAGGTACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 9056
QY      7880 GTTAATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 7939
Db      9057 CTTTATATCAATGGGGGCAATATAGTATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 9116
QY      7940 ACAACACCCGCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 7995
Db      9117 ACCCATAAAGATGTCTTCCCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 9172

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RESULT 3
US-09-873-404-3/c

Db 97396 GCCGAGCTGACGTGTCGTCGTCATCTGCGCTCACTGCACTCTCCGCTGATTC 97455
QY 10090 CTGCTAGCCTGCGGAGTCCGTCGATTCGAGCGCGGACCGCCAC 10136
Db 97456 CTGCTAGCCTGCGGAGTCCGTCGATTCGAGCGCGGACCGCCAC 97502

RESULT 7
US-09-513-999C-36203

/ Sequence 36203, Application US/09513999C
/ Patent No. 6783961
/ GENERAL INFORMATION:
/ APPLICANT: Dumas Milne Edwards, J.B.
/ APPLICANT: Duclet, A.
/ APPLICANT: Giordano, J.Y.
/ TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
/ Patent No. 6783961
/ FILE REFERENCE: 59 US, REG
/ CURRENT APPLICATION NUMBER: US/09/513,999C
/ PRIOR FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: US 60/122,487
/ NUMBER OF SEQ ID NOS: 1999-02-26
/ SOFTWARE: Patent.pm
/ SEQ ID NO 36203
/ LENGTH: 349
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 95
/ OTHER INFORMATION: y=c or t
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 96
/ OTHER INFORMATION: w=a or t
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 193
/ OTHER INFORMATION: n=a, g, c or t
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 331
/ OTHER INFORMATION: d=a or g or t
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 332
/ OTHER INFORMATION: b=c or g or t
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 333
/ OTHER INFORMATION: b=c or g or t
/ US-09-513-999C-36203

Query Match 1.0%; Score 99.8; DB 4; Length 349;
Best Local Similarity 94.4%; Pred. No. 1.1e-17;
Matches 101; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 10030 GCCGAGCTGACGTGTCGTCGTCATCTGCGCTCACTGCACTCTCCGCTGATTC 10089
Db 29 GCTGAGCTGAGCTGTCGTCGTCATCTGCGCTCACTGCACTCTCCGCTGATTC 88
QY 10090 CTGCTAGCCTGCGGAGTCCGTCGATTCGAGCGCGGACCGCCAC 10136
Db 89 CTGCTAGCCTGCGGAGTCCGTCGATTCGAGCGCGGACCGCCAC 135

RESULT 8
US-09-345-882-1/c

/ Sequence 1, Application US/09345882
/ Patent No. 6399373
/ GENERAL INFORMATION:

/ APPLICANT: Bougueterec, Lydie
/ TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-7)
/ FILE REFERENCE: GENSET.031A
/ CURRENT APPLICATION NUMBER: US/09/345,882
/ PRIOR FILING DATE: 1999-06-30
/ PRIOR APPLICATION NUMBER: US 60/091,315
/ PRIOR FILING DATE: 1998-06-30
/ PRIOR APPLICATION NUMBER: US 60/111,909
/ PRIOR FILING DATE: 1998-12-10
/ NUMBER OF SEQ ID NOS: 140
/ SOFTWARE: Patent.pm
/ SEQ ID NO 1
/ LENGTH: 162450
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 72794
/ OTHER INFORMATION: 5-124-273 : polymorphic base A or G
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 88073
/ OTHER INFORMATION: 5-127-261 : polymorphic base A or C
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 90842
/ OTHER INFORMATION: 99-1437-325 : polymorphic base A or G
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 93714
/ OTHER INFORMATION: 5-128-60 : polymorphic base deletion of GT
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 97122
/ OTHER INFORMATION: 99-1442-224 : polymorphic base G or T
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 97152
/ OTHER INFORMATION: 5-129-144 : polymorphic base deletion of T
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 99098
/ OTHER INFORMATION: 5-130-257 : polymorphic base A or G
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 99117
/ OTHER INFORMATION: 5-130-276 : polymorphic base A or G
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 103806
/ OTHER INFORMATION: 5-131-395 : polymorphic base A or T
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 106940
/ OTHER INFORMATION: 5-133-375 : polymorphic base insertion of A
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 108106
/ OTHER INFORMATION: 5-135-155 : polymorphic base insertion of A
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 108149
/ OTHER INFORMATION: 5-135-198 : polymorphic base insertion of GTTT
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 108308
/ OTHER INFORMATION: 5-135-357 : polymorphic base A or G
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 108471
/ OTHER INFORMATION: 5-136-174 : polymorphic base C or T
/ FEATURE:

RESULT 13
US-09-513-999C-16959
; Sequence 16959, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:

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; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins
; Patent No. 6783961
; FILE REFERENCE: 59, US2, REG
; CURRENT APPLICATION NUMBER: US/09/513, 999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,467
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 16959
; LENGTH: 322
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-513-999C-16959

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Best Local Similarity	94.3%	Pred. No. 9.3e-17		
Matches 100; Conservative	0	Mismatches 6	Indels 0	Gaps 0

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Db 19 ATGGCGGGCGCCCTCCCGCAGCCTCTGCTGCGCGCTTGGAGTTTGAATCTCAGCTCTGT 78
Qy 61 GCTTGCATATGACGACACTCCGTGGGGGTGAGACCTTCGAGCTAG 106
Db 79 GCTGGCAATAGCGAGACTCCGTGGGGGTGAGACCTTCGAGCTAG 124

RESULT 14
US-09-818-512-3

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1  APPLICANT: BEASLEY, Ellen et al.
2  TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
3  TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES
4  TITLE OF INVENTION: THEREOF
5  FILE REFERENCE: CU001192
6  CURRENT APPLICATION NUMBER: US/09/818,512
7  CURRENT FILING DATE: 2001-03-28
8  NUMBER OF SEQ ID NOS: 4
9  SOFTWARE: FastSeq for Windows Version 4.0
10 SEQ ID NO 3
11 LENGTH: 116592
12 TYPE: DNA
13 ORGANISM: Human
14 FEATURE:
15 NAME/KEY: misc_feature
16 LOCATION: (1)..(116592)
17 OTHER INFORMATION: n = A,T,C or G
18 IS-09-818-512-3

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Query Match	0.9%	Score 94.8;	DB 4;	Length 116592;
Best Local Similarity	93.4%	Pred. No. 1.4e-14;		
Matches 99; Conservative	0;	Mismatches 7;	Indels 0;	Gaps 0;

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60	54159	106
GCTAGCATCAGCAGCACTCTCGTGGGCGTAGAACCCTCCGAGCTAG	GCTAGCATCAGCAGCACTCTCGTGGGCGTAGAACCCTCCGAGCTAG	
54204		

RESULT 15
US-09-751-389-3/c
; Sequence 3, Application US/09751389
; Patent No. 6630334
; GENERAL INFORMATION:

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1  APPLICANT: GUEGLER, Karl et al
2  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
3  TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
4  TITLE OF INVENTION: THEREOF
5  FILE REFERENCE: CU001067
6  CURRENT APPLICATION NUMBER: US/09/751.389
7  CURRENT FILING DATE: 2001-01-02
8  NUMBER OF SEQ ID NOS: 8
9  SOFTWARE: FASTSEQ for Windows Version 4.0
10 SEQ ID NO 3
11 LENGTH: 786431
12 TYPE: DNA
13 ORGANISM: Human
14 FEATURE:
15 NAME/KEY: misc_feature
16 LOCATION: (1)..(786431)
17 OTHER INFORMATION: n = A,T,C or G
18 US-09-751-389-3

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Query Match	0.9%;	Score 94.8;	DB 4;	Length 786431;
Best Local Similarity	93.4%;	Pred. No. 5.2e-14;		
Matches 99; Conservative	0;	Mismatches 7;	Indels 0;	Gaps 0;

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Search completed: October 19, 2004, 09:50:33
Job time : 514 secs

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OM nucleic - nucleic search, using SW model

Run on: October 19, 2004, 02:09:49 : Search time 2932 Seconds
(without alignments)
17684.649 Million cell updates/sec

Title: US-10-016-248-1

Perfect score: 10136
Sequence: 1 atgcgcggcgccctccccc.....ttgcagcgcgccagccac 10136

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 3403857 seqs, 255783690 residues

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : Published Applications NA:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	7616.4	75.1	8010	16	US-10-016-248-3
3	4260.4	42.0	6004	16	US-10-016-248-38
4	2715.4	26.8	7333	15	US-10-016-248-3
5	2715.4	26.8	8034	15	US-10-016-248-3
6	2671	26.4	6409	15	US-10-016-248-3
7	2503.6	24.7	5598	15	US-10-016-248-3
8	2450.8	24.2	5667	15	US-10-016-248-3
9	2450.2	24.2	6145	15	US-10-016-248-3
10	2122.4	20.9	2487	9	US-09-799-514-3
11	1569	15.5	3810	16	US-10-108-260A-814
12	1442.8	14.2	4506	16	US-10-016-248-1
13	1371.6	13.5	2387	17	US-10-016-248-1

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15	783.6	7.7	2609	17	US-10-016-248-1	Sequence 31, Appl
16	594.8	5.9	894	15	US-10-016-248-1	Sequence 196, Appl
17	585.4	5.8	3145	16	US-10-016-248-1	Sequence 31, Appl
18	557.6	5.5	3726	16	US-10-016-248-1	Sequence 533, Appl
19	488.6	4.8	1338	16	US-10-016-248-1	Sequence 64, Appl
20	440	4.3	458	9	US-09-764-875-235	Sequence 1919, Ap
21	419.2	4.1	1581	11	US-09-764-875-235	Sequence 235, Ap
22	414.2	4.1	427	15	US-10-016-248-1	Sequence 779, Ap
23	404.4	4.0	442	10	US-09-918-995-28608	Sequence 28608, A
24	327	3.2	344	9	US-09-864-761-29585	Sequence 29585, A
25	269.4	2.7	542	9	US-09-864-761-13022	Sequence 13022, A
26	269.4	2.7	321	9	US-09-764-881-35	Sequence 35, Appl
27	269.4	2.7	321	9	US-09-764-881-35	Sequence 196, Appl
28	269.4	2.7	321	10	US-09-764-881-35	Sequence 35, Appl
29	269.4	2.7	321	11	US-09-764-881-35	Sequence 525, Appl
30	269.4	2.7	321	16	US-10-016-248-1	Sequence 91, Appl
31	234.4	2.3	1992	9	US-09-729-674-91	Sequence 91, Appl
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44	179.4	1.8	1084	15	US-10-027-632-10846	Sequence 10846, A
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ALIGNMENTS

RESULT 1
US-10-016-248-1
Sequence 1, Application US/10016248
Publication No. US20040033491A1
GENERAL INFORMATION:
APPLICANT: Alsebrook et al.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-218
CURRENT APPLICATION NUMBER: US/10/016,248
CURRENT FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: 60/254,329
PRIOR FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: 60/291,037
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 60/255,648
PRIOR FILING DATE: 2000-12-14
PRIOR APPLICATION NUMBER: 60/297,173
PRIOR FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: 60/309,258
PRIOR FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: 60/326,393
PRIOR FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: 60/315,639
PRIOR FILING DATE: 2001-08-29
NUMBER OF SEQ ID NOS: 167
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 10136
TYPE: DNA
ORGANISM: Homo sapiens
US-10-016-248-1
Query Match 100.0%; Score 10136; DB 16; Length 10136;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 301 AACGAGGGCTATATGACTCTGCAGAGGGTCCAAAGCGGATCACTGTATGAAAAGTGAAGCATG 360
Qy 361 TTTCGGGGCTGGAGCGACCAAGAGCGATCTGCGAGCCCGGATGATGATGCGCACTT 420
Db 361 TTTCGGGGCTGGAGCGACCAAGAGCGATCTGCGAGCCCGGATGATGATGCGCACTT 420
Qy 421 CGAGGGCCCTCGGAGCATATCACTCTCCCAATTTCCCATTCAGTATGACAACAATGA 480
Db 421 CGAGGGCCCTCGGAGCATATCACTCTCCCAATTTCCCATTCAGTATGACAACAATGA 480
Qy 481 CACTGTGTGTGATCATATCAGACATCCCTCCAGAGTATCAAGCTCGCTTTGAG 540
Db 481 CACTGTGTGTGATCATATCAGACATCCCTCCAGAGTATCAAGCTCGCTTTGAG 540
Qy 541 GAGTTGATTTGGAGAGGGGCTATGACCCCTGACGGTGTGATGATGATGATGAG 600
Db 541 GAGTTGATTTGGAGAGGGGCTATGACCCCTGACGGTGTGATGATGATGATGAG 600
Qy 601 GACAGAGAGAGAGTTCTTACATGTCTCAAAATGCTGAGTGAAGCCCTCAACCCCA 660
Db 601 GACAGAGAGAGAGTTCTTACATGTCTCAAAATGCTGAGTGAAGCCCTCAACCCCA 660
Qy 661 GGGCTTCGCAATCCCAAGAGCATGTCTGGGGACATCTGAGAGGAGAAATGACTGTACT 720
Db 661 GGGCTTCGCAATCCCAAGAGCATGTCTGGGGACATCTGAGAGGAGAAATGACTGTACT 720
Qy 721 GAGATGTGTGATGAGAGTTGAGATGAGAGTTGAGAGTTGAGAGTTGAGAGTTGAG 780
Db 721 GAGATGTGTGATGAGAGTTGAGATGAGAGTTGAGAGTTGAGAGTTGAGAGTTGAG 780
Qy 781 AAGACTTCTAATGCTGTGAGAACTTTGCTCTGAGGACAGAGTCAAGAGGCACTTGC 840
Db 781 AAGACTTCTAATGCTGTGAGAACTTTGCTCTGAGGACAGAGTCAAGAGGCACTTGC 840
Qy 841 GGTGACCTTGGCATATCTGATATGAGCCGAGAGGAAAGGCTCCCGGTTTCAACAGGTTGAC 900
Db 841 GGTGACCTTGGCATATCTGATATGAGCCGAGAGGAAAGGCTCCCGGTTTCAACAGGTTGAC 900
Qy 901 AACTCAAGTTGAGAGGCGACCCGCTTGAAGCTGTGAGGAGAGAGAAAGCAATCAATGC 960
Db 901 AACTCAAGTTGAGAGGCGACCCGCTTGAAGCTGTGAGGAGAGAGAAAGCAATCAATGC 960
Qy 961 CAAAAGAAATTAACAATGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
Db 961 CAAAAGAAATTAACAATGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
Qy 1021 TTTCACAGCCGCTGTGGGGTGTCTGTCTCTCCCACTCCAGAGAGATATGAGCAAC 1080
Db 1021 TTTCACAGCCGCTGTGGGGTGTCTGTCTCTCCCACTCCAGAGAGATATGAGCAAC 1080
Qy 1081 CTTCACATGTGTCTGTGATCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
Db 1081 CTTCACATGTGTCTGTGATCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
Qy 1141 GACATTTGAG 1200
Db 1141 GACATTTGAG 1200
Qy 1201 GGGCCGCTCTGTGGGCACTTTCTCAGAGAAACAGCTTCCCTCTCCATCAACAGCACTGAC 1260
Db 1201 GGGCCGCTCTGTGGGCACTTTCTCAGAGAAACAGCTTCCCTCTCCATCAACAGCACTGAC 1260
Qy 1261 CAGCTGCGCGCTGTGAGTTCCAGACTGACACTTCCACAGAGAGAGAGAGAGAGAGAG 1320
Db 1261 CAGCTGCGCGCTGTGAGTTCCAGACTGACACTTCCACAGAGAGAGAGAGAGAGAGAG 1320
Qy 1321 ACTTTTACACCTTCCGACACAAGAGTCCGAGATCTGAGCTTCAAGTAAATGAGCAAA 1380
Db 1321 ACTTTTACACCTTCCGACACAAGAGTCCGAGATCTGAGCTTCAAGTAAATGAGCAAA 1380

Db 1321 ACTTTTACACCTTCCGACACAAGAGTCCGAGATCTGAGCTTCAAGTAAATGAGCAAA 1380
Qy 1381 CGGTTTGGGGAACAGCTTCCAGCTGGGAGAGTCCATCTCTCTCTGTGATGAGAGCTTC 1440
Db 1381 CGGTTTGGGGAACAGCTTCCAGCTGGGAGAGTCCATCTCTCTCTGTGATGAGAGCTTC 1440
Qy 1441 CTTGGGACTCAGAGGCTCAGAGACCAATCACTGCGTCTGAGAGAGAGAGAGAGAGAG 1500
Db 1441 CTTGGGACTCAGAGGCTCAGAGACCAATCACTGCGTCTGAGAGAGAGAGAGAGAGAG 1500
Qy 1501 AACAGGCTGTGTGTGAGAGTCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1560
Db 1501 AACAGGCTGTGTGTGAGAGTCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1560
Qy 1561 ACCATCTCTCTCCGGGCTGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1620
Db 1561 ACCATCTCTCTCCGGGCTGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1620
Qy 1621 ATTGAGGCCAGAGAGGCTTACCCCATCAAAATCACTTGCAGAGATTCAAAACGAGATC 1680
Db 1621 ATTGAGGCCAGAGAGGCTTACCCCATCAAAATCACTTGCAGAGATTCAAAACGAGATC 1680
Qy 1681 AACTATGACACCTGTGAGAGTACGCGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
Db 1681 AACTATGACACCTGTGAGAGTACGCGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
Qy 1741 TACAGAGGAGCCAGAGTTCCTCCAGTTCCTCATACAGACAGCACTTACTTCTCTCT 1800
Db 1741 TACAGAGGAGCCAGAGTTCCTCCAGTTCCTCATACAGACAGCACTTACTTCTCTCT 1800
Qy 1801 TTCTTACAGAGAGAGTCACTCGAGATCGAGCTTCACTCGAGTGTGAGTGTGAGTGTGAG 1860
Db 1801 TTCTTACAGAGAGAGTCACTCGAGATCGAGCTTCACTCGAGTGTGAGTGTGAGTGTGAG 1860
Qy 1861 CTGCAATGACACACTGT 1920
Db 1861 CTGCAATGACACACTGT 1920
Qy 1921 GACTTCTAAGTGTGGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1980
Db 1921 GACTTCTAAGTGTGGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1980
Qy 1981 GGGGAGGCTCTGAGAGTGTGAGGCGCACTTCAAGTGTGAGGCGGAGGCTGTGAGTGTGAG 2040
Db 1981 GGGGAGGCTCTGAGAGTGTGAGGCGCACTTCAAGTGTGAGGCGGAGGCTGTGAGTGTGAG 2040
Qy 2041 GCTCTGT 2100
Db 2041 GCTCTGT 2100
Qy 2101 GACTTCTAAGT 2160
Db 2101 GACTTCTAAGT 2160
Qy 2161 GTGTCTTCACTTGT 2220
Db 2161 GTGTCTTCACTTGT 2220
Qy 2221 GAGAGGAGAGGCTTACCCAGGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2280
Db 2221 GAGAGGAGAGGCTTACCCAGGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2280
Qy 2281 ATCAGGCTGT 2340
Db 2281 ATCAGGCTGT 2340
Qy 2341 ATGTCAATGAGAGAGATTCAACATCACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2400
Db 2341 ATGTCAATGAGAGAGATTCAACATCACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2400
Qy 2401 CCCGAGGCTCCAGGCTTACAGATCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2460
Db 2401 CCCGAGGCTCCAGGCTTACAGATCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2460

QY	3541	GAAATCAGCTGTGTGAAGATCGAGAA	CAGAGTCTTCTGCGACGCCAGCCGCAACATG	3601
Db	3541	GAAATCAGCTGTGTGAAGATCGAGAA	CAGAGTCTTCTGCGACGCCAGCCGCAACATG	3601
QY	3601	ATGCGTTCCTCGGGGGAGAACTTGA	CAGGACCATCTGAGTATCTCTCA	3661
Db	3601	ATGCGTTCCTCGGGGGAGAACTTGA	CAGGACCATCTGAGTATCTCTCA	3661
QY	3661	CCAGAACCCCTAACCCCGCAGGCAAG	AGATGTGCTGAAAATGACACCGTCTCACACAACTAC	3722
Db	3661	CCAGAACCCCTAACCCCGCAGGCAAG	AGATGTGCTGAAAATGACACCGTCTCACACAACTAC	3722
QY	3721	GTATCGCCCTGTGATTTTAACTTTAA	CTTTTAACTGAGCCTGGCTATGACTTCTCTCCATATC	3780
Db	3721	GTATCGCCCTGTGATTTTAACTTTAA	CTTTTAACTGAGCCTGGCTATGACTTCTCTCCATATC	3780
QY	3781	TACGACGGAGCGGGACTCTCTCA	AGCCCTCTCATAGAAAGCTTATAGCTCTCCAGCTCCCA	3840
Db	3781	TACGACGGAGCGGGACTCTCTCA	AGCCCTCTCATAGAAAGCTTATAGCTCTCCAGCTCCCA	3840
QY	3841	GGCCCGCATTTGAAGAGCAGCAGCA	CAGCCTCTTCCTCGCTTCGCGAGAGATGACATCTGTG	3900
Db	3841	GGCCCGCATTTGAAGAGCAGCAGCA	CAGCCTCTTCCTCGCTTCGCGAGAGATGACATCTGTG	3900
QY	3901	AGCAATGCTGGCTTGTGTAATTA	CTATATCAGAAAAACCGCGGAGATCATGTTTTGATCT	3960
Db	3901	AGCAATGCTGGCTTGTGTAATTA	CTATATCAGAAAAACCGCGGAGATCATGTTTTGATCT	3960
QY	3961	GGTTCCATCAAGAAAGGACAGGACA	CGGGTGGGGTCCGACCTGMAAGCTGGGCTCTCTCGTCAAC	4020
Db	3961	GGTTCCATCAAGAAAGGACAGGACA	CGGGTGGGGTCCGACCTGMAAGCTGGGCTCTCTCGTCAAC	4020
QY	4021	TACTACTGCCACGGGGGCTGAGAA	GTGAGGGCACCTTGACCCCTGAGCTGATCTCTGGGG	4080
Db	4021	TACTACTGCCACGGGGGCTGAGAA	GTGAGGGCACCTTGACCCCTGAGCTGATCTCTGGGG	4080
QY	4081	CCTGATGGGAAAGCCCGTGTGGA	AAATCCCGGCAATCTGACAAGCCCTGTGGGGGA	4140
Db	4081	CCTGATGGGAAAGCCCGTGTGGA	AAATCCCGGCAATCTGACAAGCCCTGTGGGGGA	4140
QY	4141	CAGATATGAGGTTCCGACGAGATG	GTGTTTCCCCCAATCCACCCCGCAATCAACAGT	4200
Db	4141	CAGATATGAGGTTCCGACGAGATG	GTGTTTCCCCCAATCCACCCCGCAATCAACAGT	4200
QY	4201	GGAAGATCTGCTCTGATATTTTGT	TATCTGTCGCGCAAGACTATGTGTTGGCAGTTC	4260
Db	4201	GGAAGATCTGCTCTGATATTTTGT	TATCTGTCGCGCAAGACTATGTGTTGGCAGTTC	4260
QY	4261	GCTTCTTTTCAACGCGCCCTCA	ACGACGTGTGGAAGGTTCAAGACGCGCAACGCGACAC	4320
Db	4261	GCTTCTTTTCAACGCGCCCTCA	ACGACGTGTGGAAGGTTCAAGACGCGCAACGCGACAC	4320
QY	4321	TGCGGGCTCCTCAGACTCCCTCT	CGGGGTCCCATACAGGAATCATCTGCCCTTGGCACC	4380
Db	4321	TGCGGGCTCCTCAGACTCCCTCT	CGGGGTCCCATACAGGAATCATCTGCCCTTGGCACC	4380
QY	4381	TCCAAATCAAGTTCATTAAGTTA	AGTTCAAGGCGCAAAAGGCTGTGCACACAGAGGCTTCCAC	4440
Db	4381	TCCAAATCAAGTTCATTAAGTTA	AGTTCAAGGCGCAAAAGGCTGTGCACACAGAGGCTTCCAC	4440
QY	4441	TTTTGTCTAACCAACGGTTCCT	CGMACACAGCCACGCACTGACAGCTCTGTGCCGAAACC	4500
Db	4441	TTTTGTCTAACCAACGGTTCCT	CGMACACAGCCACGCACTGACAGCTCTGTGCCGAAACC	4500
QY	4501	CGCTATGACCAAGAGGCTGGCAG	GTGACTTCTCTCGTGGGGCCATGTCGCTTCGAAATGC	4560
Db	4501	CGCTATGACCAAGAGGCTGGCAG	GTGACTTCTCTCGTGGGGCCATGTCGCTTCGAAATGC	4560
QY	4561	AACCTCGGCTATGCTCCCTG	CAGGGGTTGCCAGAGATCTGATGCTCCCTGTGCTGGGGCC	4620
Db	4561	AACCTCGGCTATGCTCCCTG	CAGGGGTTGCCAGAGATCTGATGCTCCCTGTGCTGGGGCC	4620
QY	4621	TTGGCCCAATGAATGTCTCA	CGCCCACTGTGTGTGGTGCCTGTGAGGCAACTCTACA	4680

Db 4621 TTGGCCCAATGAAATGCTCAGCGCCACAGTGTGTGCTGCTGAGGCAACCTTCACA 4680
Qy 4681 GAGCGCAGAGGGGCACATCTCTGTCCCTGGTCTCCAGAGCCGTAACCTCAACAGCTTCAC 4740
Db 4681 GAGCGCAGAGGGGCACATCTCTGTCCCTGGTCTCCAGAGCCGTAACCTCAACAGCTTCAC 4740
Qy 4741 TGTGTGTGAAAGATCGTGTGCTCCCGAAGAGGCTGGATCCAGATCCAAAGTTTCAGTTT 4800
Db 4741 TGTGTGTGAAAGATCGTGTGCTCCCGAAGAGGCTGGATCCAGATCCAAAGTTTCAGTTT 4800
Qy 4801 GTGACAGACAGAACTGGAGACTGCTGAGATATTTGATGTGTGACAGATTAACACTGTAAAC 4860
Db 4801 GTGACAGACAGAACTGGAGACTGCTGAGATATTTGATGTGTGACAGATTAACACTGTAAAC 4860
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Db 4861 ATGTCTGGGAGTTTCTCAGGAAACAACCTGTCCCTTGTGAACAGCACTTCACACAG 4920
Qy 4921 CTCTACTTCAATTTCTACTCAGATATCAGGCTATCAGAGCTGGCTTCCACTTGGAGTAC 4980
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Db 5521 CCAGACCCAGAGGCTTTCGCAATGAGGAGGAGCTGGCTACAAAGTGGAGCA 5580
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Db 5821 CTCAGGCTCTGACAGAGAGCCCTCTGAGATTTTATCATCCATCTGGAGTGGAGCCACAG 5880
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Qy 6061 GAAAGTGTACAGAGATGAAAGATTCATATATAGTGAATGTAAGTATCAGATGCTC 6120
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Db 6301 TCTTGGCTGTGAGATGAGTGAAGCCGACTTAAATCTCCCTCAACATGAGTACTTCC 6360
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 DB 7288 ----- 7287
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 DB 7459 GTGC----- 7462
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 DB 7621 GAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 7680
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 US-10-467-433-38
 ; Sequence 38, Application US/10467433
 ; Publication No. US2004008773A1
 GENERAL INFORMATION:
 ; APPLICANT: INCYTE CORPORATION;
 ; APPLICANT: LAU, Preeti G.; BAUGHN, Mariah R.;
 ; APPLICANT: YAO, Monique G.; CHAMLA, Narinder K.;
 ; APPLICANT: ELIOTT, Vicki S.; XU, Yuning;
 ; APPLICANT: HONCHILL, Cynthia D.; YUE, Henry;
 ; APPLICANT: DING, Li; GRETZEN, Kimberly U.;
 ; APPLICANT: ISON, Craig H.; LU, Dyrung Aina M.;
 ; APPLICANT: HAPALIA, April J.A.; GANDHI, Ameena R.;
 ; APPLICANT: THANGAVELU, Kavitha; SANJANMALA, Madhusudan M.;
 ; APPLICANT: TANG, Y. Tom; RAMKUMAR, Jeyalaxmi;
 ; APPLICANT: GRIFFIN, Jennifer A.; SWARNAKAR, Anita;
 ; APPLICANT: AZIMZAI, Yalda; SAPPERSTEIN, Stephanie K.;
 ; APPLICANT: BURFORD, Neil; LEE, Ernestine A.;
 ; APPLICANT: LU, Yan; TRAN, Uyen K.;
 ; APPLICANT: MARQUIS, Joseph P.
 TITLE OF INVENTION: MOLECULES FOR DISEASE DETECTION AND TREATMENT
 FILE REFERENCE: PF-0899 USN
 CURRENT APPLICATION NUMBER: US/10/467,433
 PRIOR FILING DATE: 2003-08-06
 PRIOR APPLICATION NUMBER: PCT/US02/03709
 PRIOR FILING DATE: 2002-02-08
 PRIOR APPLICATION NUMBER: US 60/268,117
 PRIOR FILING DATE: 2001-02-09
 PRIOR APPLICATION NUMBER: US 60/269,618
 PRIOR FILING DATE: 2001-02-15
 PRIOR APPLICATION NUMBER: US 60/271,118
 PRIOR FILING DATE: 2001-02-23
 PRIOR APPLICATION NUMBER: US 60/274,486
 PRIOR FILING DATE: 2001-03-07
 PRIOR APPLICATION NUMBER: US 60/274,436
 PRIOR FILING DATE: 2001-03-09
 PRIOR APPLICATION NUMBER: US 60/334,229
 PRIOR FILING DATE: 2001-11-28
 PRIOR APPLICATION NUMBER: US 60/353,284
 PRIOR FILING DATE: 2002-02-01
 NUMBER OF SEQ ID NOS: 40
 SOFTWARE: PERL Program
 SEQ ID NO 38
 LENGTH: 6004
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc feature
 OTHER INFORMATION: Incyte ID No: 55061615CB1
 US-10-467-433-38
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Matches 3952; Conservative 0; Mismatches 1879; Indels 84; Gaps 3;

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RESULT 5
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 ; Sequence 6, Application US/10276934
 ; Publication No. US20030180750A1
 ; GENERAL INFORMATION:
 ; APPLICANT: University of Leeds
 ; APPLICANT: Marham, Alexander F.
 ; APPLICANT: Jackson, Andrew P.
 ; APPLICANT: Woods, Christopher G.
 ; TITLE OF INVENTION: Treatment of Cancer and Neurological Diseases

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FILE REFERENCE: 9052-144
CURRENT APPLICATION NUMBER: US/10/276,934
CURRENT FILING DATE: 2002-11-20
PRIOR APPLICATION NUMBER: PCT/GB01/02240
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PRIOR FILING DATE: 2000-05-20
NUMBER OF SEQ ID NOS: 16
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DB 4574 TACAGTTGCAACCGGGGTAGCGCTATGATGAGCAACCTGTACGTGTGTGAGTGA 4633
QY 3043 GAGGCGGAGCTTGGGACCGGCTCTGCGCACTGTGTGCGCAGATGTGAGGAGACAGT 3102
DB 4634 GACGAGAGATGTGGGACCAACCACTACCTTGTGATAGCGGAATGTGTGTGATC 4693
QY 3103 AGAGGAGAGTGTGGGAGAGTGTGTGACCGGCTATCCAGCTCTCTATGAACAAT 3162
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DB 4754 CTCACTGTGACCTGTGATTAAGGAGACCAAGAAAGCAATTAAGCTTCCATTTCAAT 4813
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DB 4814 GTTTGACACAGGATGTGCTCAAGATCTCAAGTCTGGGAGCGGCGGATGACAGT 4873
QY 3283 GGGGTTCTGTGAAGAGCTGAGTGGCGGCGCTGCGCAAGGACTGTGATAGCACTTTC 3342
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QY 3403 CAATTTTCACTGTCAAGCAAGTCTTCAATGACCTGTGAGTCCGAGATGAGGAGT 3462
DB 4994 CAGTTTCACTCAATTCAGCACTGTATCAAGATCCAGATGAGGAGGAGGAGT 3522
QY 3463 CGGAGTGTGAGAGTGTGGAAGCGGCGACCTCAAGTGTTCAGATGAGACCTTGCATC 3522
DB 5054 CGGTATGAGAGAGCAAGAGGCTGAGACACCTGTCACTTCAATGTGAGACCTTGCATC 5113
QY 3523 GCGCTGACAGGAAGTGCAGAGATCAGTGTGTGAAGATGAGAACAGGTTCTTGGCAG 3582

Db 5114 CAGCTCCAAAGGCAAGCAAAATCACCTGTGTGACGTGATTAACGGGTTCTTTGGCAA 5173
 Qy 3583 CCCAGCCCCGCAATGATCGCTCCCTCGGGGGAGACTGACAGACCATTTGGAGTC 3642
 Db 5174 CCAGACCTCTCTAATGATAGCTGTGTGGAGGAATCTGACGGGCCAGAGAGGTGT 5233
 Qy 3643 ATCTCTCAACAAATTAACCGAACCCTACCGCCAGGCAAGGAGTGTGCTGGAAAGTG 3702
 Db 5234 ATTTGTACACCACTACACAGCGGTATCTCTGGAGGAAGTGTGCTGGAGATGA 5293
 Qy 3703 ACCGTCTCAACAGACTACGTATCGCCCTGTGATTTTAACATCTTTAACCTGAGCCCTGCG 3762
 Db 5294 AAGTGAACCCGAGCTTTGTGATCGCTTGTATTAAGATTCAACATGAGGCCAGG 5353
 Qy 3763 TATGACTTCTCTCAATCTAAGACGAGCGGAGCTCTCTAGCCCTCTCATAGAGCTTC 3822
 Db 5354 TATGACTTCTCTACATCTATGAAGGGGAGATTTCCACAGCCCCCTCATTTGGGAGTTAC 5413
 Qy 3823 TATGCTCCAGCTCCAGGCGCATTTGAAGAGAGAGCAAGCCCTCTCGGCTTC 3882
 Db 5414 CAGGGCTCTAGGCCCCGAAAGAAATAGAGATAGCGAAACAGCTGTTCTGGCATTT 5473
 Qy 3883 CGCAGCGATGATCTGTGACAAATGCTGCTTGTGATTTGATTAACAGAAACCCGCG 3942
 Db 5474 CGAGATGATGCTCCGTTGGGCTTTGAGGTTGCGCATTTGAATTAAGAGAAACACG 5533
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 Qy 4063 CTGAGCTGATCTCTGGGGCTGTATGGGAAAGCCGTGTGAAACATCCCGGCGCATCTG 4122
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 Qy 4123 ACAGCCCCCTGTGGGGAGAGATGTGGGTTGCGAGCGAGTGTCTTTGCCCCAACTAC 4182
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 Db 6014 TCTGCCGCGGCTTTCACCTTGTGTATCAAGCTGTCTCTGTACAGATGACACCCATGCG 6073
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 Qy 4543 ATGTGCTTTCGAATGCAATCTCGGCTATGCTGTGAGGGGTGCGCAGAGATCGAGTGC 4602
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 Db 6674 GAGCCGGGTAACACTGTGAGGCGCTTCCACATTTCTGTATGTGAGGAGCGCTGAGCACTTG 6733
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 Qy 5203 GAGGGGTATCTGTAGGCGCGGCTTCCAGGCACTACCCAGTAACTATGATCTGTCTCC 5262
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 Qy 5263 TGGAAATATGACCTGCGGCTTGTGAGCTCACTCAAGTCTCTGAACTTCTGACC 5322
 Db 6854 TGGAGATCTCACTTACCCATCGGCTATGTGTGACATATTCAGTTTGTGAATTTTCTAAC 6913
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 Db 6914 GAAGTAAATCATGACTCTCTGAAATTAAGATGAACTTACCAACAGCGCCCATGATTT 6973
 Qy 5383 GGAAGATTCAGTGGAAGCAAGCTTCCAGCTCCCTCTCTCCAGTGTCCACAGAGACAC 5442
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Db	7334	TTTCTGTAGAGTATCCGATCTGTGAAGACGTGCATTATTTGGCTATCAACGTCCTCCACGGG	73939
OY	5803	CATGGCGTCCGCTCAACCTCAGCCTGTGCGAGACAGACCCCTGAGAGATTTTCATCAC	58628
Db	7394	CACGGAGTTTACATCAACTTCAACCTGTTAACGACGGAAGGTGTCAACGATTTACATTGCT	74533
OY	5863	ATCTGGATGGGGCCACAGCAAAACAGACACACGAGCTCGGCGCTTTCACCCGAGCATGGCC	59222
Db	7454	GTTTGGGACGATCCCGATCAGAACTCACCCACGCTGGGAGTTTTCAGTGGCAACACAGCC	75133
OY	5923	AAGAAAACATGTCAGAGATTCAATCAACAGGATCTGTCAAGTTTCAACCTGATGACGCC	59882
Db	7514	CTCGAAACGGGATAGCTCCACCAACCAATCTCGGTCAAGTTCCAAAGGACCTTTTCA	75733
OY	5983	ACAGGGGGGATCTTGCCCATAGAGCTTTCCCGCTTA	6017
Db	7574	AATGGAGCTTCTTTGCTCTCAATTTCCACGGTCA	7608

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RESULT 6
US-10-276-934-3
; Sequence 3, Application US/10276934
; Publication No. US20030180750A1
; GENERAL INFORMATION:
; APPLICANT: University of Leeds
; APPLICANT: Marham, Alexander F.
; APPLICANT: Jackson, Andrew P.
; APPLICANT: Woods, Christopher G.
; TITLE OF INVENTION: Treatment of Cancer and Neurological Diseases
; FILE REFERENCE: 9052-144
; CURRENT APPLICATION NUMBER: US/10/276,934
; CURRENT FILING DATE: 2002-11-20
; PRIOR APPLICATION NUMBER: PCT/GB01/02240
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: GB0012186.3
; PRIOR FILING DATE: 2000-05-20
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 6409
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (588)..(588)
; OTHER INFORMATION: "n" is any nucleotide
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (624)..(624)
; OTHER INFORMATION: "n" is any nucleotide
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (672)..(672)
; OTHER INFORMATION: "n" is any nucleotide
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2265)..(2265)
; OTHER INFORMATION: "n" is any nucleotide
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (6387)..(6387)
; OTHER INFORMATION: "n" is any nucleotide
US-10-276-934-3

Query Match      26.4%; Score 2671; DB 15; Length 6409;
Best Local Similarity 66.8%; Pred. No. 0;
Matches 3895; Conservative 0; Mismatches 1854; Indels 84; Gaps 3

OY      185 TAACTAGGTGGTGTGTCCCAAGACATATATATGTGTCCAGACCCCTGGCATCCCGAAT 244
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Db	236	TAGGCCAAGAGGCTTTGCAATGTGCTCTGACATGTTGTCCAGATTCCTGGGATTTCCAGAAA	235
QY	245	GGGGCAAAAGACTAGGCTCGGATTTTCAGGTTAGGATCCAGCCTCAAGCTTCAGCTTCGCAACG	304
Db	296	ATGTGTAGAAAGAGAGGTTCCGACCTTCAAGGGTGTGTGCAAAATGTAACAGTTTTCATGTGAGG	355
QY	305	AGGGCTATGACTTCGCAAGGGGTCCAAACCGATCTCACTGTATGAAAGTGAAGGACATGTTTG	364
Db	356	ACAATTACGTCTCCAGGGATCTTAAAGCATCACTGTAGAGAGTATACAGAACCTCG	415
QY	365	CGGCTTGGAGCGACCAAGGCCAGTCTGCCAGGCCGATGTGTGATGCCCACCTTCGAG	424
Db	416	CTGCTTGGAGTGACCAAGGCCCATCTGCCAGCGAGAACATGTGATTCCAATCTGCTG	475
QY	425	GGCCCTCCGGCATTCACTCACTCTCCCAATTTTCCCATTTCAATATGCAACATGACACT	484
Db	476	GGCCCAAGCGCGCATTTACTCTCCCTCAATTATTCGGTTCAATGAAAGTAAATGACACT	535
QY	485	GTGTGTGATTCATCAAGCACTCAACCCCTCCAGAGGTGATCAAGCTCGACTTTAGGAGT	544
Db	536	GTGTGTGGGTATCAACCAACCAAGCCGGAACAGTCAATCAAGCTTGTCTTNGAAGAT	595
QY	545	TTGATTTGGAAGAGGGCTATGCAACCTGACGGTCCGTGATGTGTGATGGAATGGGAC	604
Db	596	TTGAGCTGGAAGGAGGCTATGACACCTTACGGTTGTGTGATCTGGGAAAGTGGGAGACA	655
QY	605	AGAAAGCAGTTCTCTCAATGTCTCAAAATGCTGCAAGTACAGCCCTCACACCCAGGT	664
Db	656	CCAGATCGGTCTTTGATNGCT-----CACGGAT	685
QY	665	CTGCGATCCCAAGAGCAATGTCTGGGACATCTGAGGACAGAAATGACCTGATCTTGAGA	724
Db	686	CCAGGTCTCTGACCTCAT---TGTGACATGAGCAACAGATGTGGCTACATCTGACGT	742
QY	725	TCGTGTGAGCAATTGACAGTTCAATGCAATGCAAGTCAAGTTCAGTGAGGAATCTCCAAAGA	784
Db	743	CGGATGATAGCATTTGGC-----	759
QY	785	CTTCTAATGCTGTGGAATTGTTGCTCCTGGGACAGAGATCGAGGAGGCAAGTTGCGG	844
Db	760	-----TCACCTGGTTTAAAGTGTTTACAAAGAAATTGAAAGGAGGAGTGTGGG	811
QY	845	AACCTGGCATACCTGCATATATGGCCGGAAGGAAGCTCCCGGTTTCCACGCTGACAC	904
Db	812	ATCTCGAGATCCCGCCTATGAGGAAGCGAGCGGGACAGATTTCTTCATGAGATGAC	871
QY	905	TCAAGTTTGAATGTCAGGCGCGCTTTGAGTGTGTGGGACAAAGGCAATCAATGCCAA	964
Db	872	TCACCTTTGAAATGCCCGCGGCTTTGAGCTGTGTGGGAGAGATTATCACCTGTGACG	931
QY	965	AGATTAACCAATGTCGGCTAAGAAGCCAGGCTGCGTTCCTGCTTCTTCAACTTCA	1024
Db	932	AGAACAAATCAATGTGCTGGCAACAGCCACAGCTGTGATTTTCAATGTTTCTTCAACTT	991
QY	1025	CCAGCGCGTGGGGGTGTCTGTCTCCCACTTCCAGAGGATATATGGACCAACACTTCC	1084
Db	992	CGGATATATCTGGGATTAATTTCTGTCACCAATTAATCCAGAGGAATATGGAACAACATGA	1051
QY	1085	ACTGTGTCTGCTCATCTGTCCAGGCGCTGAGGCCCATTCACCTGAGCTTCAACGACA	1144
Db	1052	ACTGTGTCTGGTTATATCTCGGAGCCAGGAAGTGAATTCACTTAATCTTTTAAATGTT	1111
QY	1145	TTGACGTGAGACCTCAAGTTGATTTCTGTGATCAAGAAATGGGGCCACCGCGAGGCGC	1204
Db	1112	TTGATGTTGAGCTCAATTTGACTTTCTCGCGTCAAGATGATGTCATTTCTGACATAA	1171
QY	1205	CCGTCTTGGGACCTTCTCAGAGAAACAGGCTTCCCTCTCATCAACAAAGAGTGGCCAGC	1264
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QY	1265	TGGCCGCTCTGAGTTTCAAGCTTGAACCTTCAACAGGAAGAGGGCTTCAACATCACTT	1324
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OY	1325	TTACCACTTCCGACACACACAGATGCCGGATCTCTGGGCTCCAGTAATATGGCAAGGCT	1384
Db	1292	ACACCACATTTGGTCTCAGATAGATGATGCCATGATCTCGGATTCCTATAAACGACGAGTT	1351
OY	1385	TTGGGGACAGCCTCAGCTGGGACAGCTCCATCTCTCTCTGTGATGAAGCTTCCGTG	1444
Db	1352	TTGGGTGACAGGTTTCTACTCCGGAGCTCGGTTTCTTTCCACTGTGATGATGGCTTTGTCA	1411
OY	1445	GGACTCAGGGCTCAGAGACATCACTTGCGTCTTGAAAGAGGGACCGTGTCTTGACAA	1504
Db	1412	AGACCCAGGATTCGAGTCCATTTACTGTCATATGACAAAGGGAAAGTGTCTGGAGCT	1471
OY	1505	GCGCTGTCTGGGCTGTGAAGCTCCCTGTGTGGTCACTGACTTTCGCCACGGCCACCA	1564
Db	1472	CCACCGTCCCCCGCTGTGAAGCTCCATGTGGTGGACATGTACAGCGTCCACGGAGTCA	1531
OY	1565	TCCTCTCCGGGCTGGCGCTGCTCTTCAAGAGATGCTTGAGCTGTGGCTCGGATGTG	1624
Db	1532	TTTGGCTCTCGGATGGCCAGAGATTTATTAAGGATCTTTTACATTGGAAATGATTAATG	1591
OY	1625	AGGCCACGACAGGCTACCCCATCAAAATCATCCTTGCAGATTCAAAAACGAGGTCACT	1684
Db	1592	AAGCAAACACAGGCCACCTCTATCAAAATAACTTTTGACAGATTTCCAGACAGGTCAATT	1651
OY	1685	ATGACACCCCTGGAATGACGCGATGGGCGGAACTTACTCAGCGCCCTTGATCGGGGTTTACC	1744
Db	1652	ATGACACCTTGAGAGGTGAGAGATGGGCGACGACAGTTGCTCCCATGTATGGCGAGTACC	1711
OY	1745	ACGGGACCCAGGTTTCCCATGTTCTCTATCAGACACAGCAATCTACTCTCTCTTCT	1804
Db	1712	ACGGCACCCAGGACCCCGAGTTCTCCATCAGACACGGGAACTTCAATGACTCTGTAATYCA	1771
OY	1805	CTACCGACAAAGTCACTCGGACATCGGCTTCCAGCTCCGGCTATGAGACTATACTGTC	1864
Db	1772	CCACTGACAAACAGCCGCTCCAGCATCGGCTTCTCATCTATGATGATGTGACGCTTG	1831
OY	1865	AGTCGACCACTGTCTGTGATCCAGGAATCCAGTAATGACAAGCGTCAATGGGAATGACT	1924
Db	1832	AGTCGGAATTCCTGGCTGGACCCGGGCATCTCGTGAAAGGCGCATGCGCAGCGTGAAGCT	1891
OY	1925	TCCTACGTGGGCGCGCTGGTACCTTCAAGCTGTGACTCGGGCTACACATTAAATGAACGGG	1984
Db	1892	TTGGCATGAGGTCCACAGTGACTTTCAGCTGTGACCCGGGGTACACACTAATGATCAGACG	1951
OY	1985	AGCCCTGAGATGAGGCCCAACTTCCAGTGAAGCCGGGCCCTGCCAGTTGTAAGCTC	2044
Db	1952	AGCCCTGCTGTGTAGAGGAACACACAGTGAACACGCTTGCACGCTGACACGCTC	2011
OY	2045	TCGTGTGTGCTTCACTTCAAGGCTCCAGTGGGACCATCTTGTGCCAGGGTTCCTGACT	2104
Db	2012	TATGTGAGGCTACTCATCCAGGAAAGATGGAACAGTCTCTTCTCTGGGTTTCCAAATT	2071
OY	2105	TCCTACCCCAACAACTTGAAGTGCACCTGGAATTAATGAAAATCTCATGGCAAGGCTGT	2164
Db	2072	TTTATCCAACTCTTAATAGCAGCTGACCATTTGAAGTGTCTCATGGGAAAGAGTTC	2131
OY	2165	TCCTTCACTTTCACACCTTCCACTGGAAATGGGCGATGACTACTCCTCATCACTGAGA	2224
Db	2132	AAATGATCTTTCACACCTTTCATCTTGAAGTTCCTCCAGCTATTATTCTGATCCAAAGG	2191
OY	2225	ACGGCAGCTTACCCAGGCCCTGAGGAGGACGTAACTGGAATCCGGGTGCAGCTCCCATCA	2284
Db	2192	ATGGAAGTTTTCGAGGCCGTTGCCAGGCTCACCGGGTCCGATGTGCTTATACATCA	2251
OY	2285	GCGCTGGGCTGTATGGCACTTCACTGCCCCAGTCCGCTCTCATCTGTATTCTTCCATGT	2344
Db	2252	AGGCAAGCCTGTGTGGAAATTTCACTGCCACAGCTTCGGTTTATATACAGACTTTCATATT	2311
OY	2345	CATATGAAGATTCACACATCACTTCTAGAGTACAGCTTGGAGCCTGTGAGAGCCCG	2404
Db	2312	CGTAGAGGGCTTCAATATCAATTTTACAGATATGACCTGGAGCCATGTGATATCTGT	2371

QY	2405	AGGTCCAGCCTTAACAGCATCCGGAAAGGGCTTGACGTTTGGGTGGGGAGACCTTGACCT	2464
Db	2372	GAGTCCCTGCCTTCAGCCGAAAGTTGGTTTCACTTTGGGTGGGAGACTCTCTGACGT	2431
QY	2465	TCTCCGTGTTCCCGGGGATCCGTCTGGAGGGGCAACGCGCCGCATCAGCTGCCTGGGGGGCA	2524
Db	2482	TTTCTGCTTCTCTGGGATATGTGTTTAGAGGTGCACCAAGCTTACCTGCTGGGTGGG	2491
QY	2525	GACGCGCCTTGGAGCTCGCTCTGCGCAAGTGTGTGCTGAGTGTGGAAATTCACTCA	2584
Db	2492	GCCGCGGTGTGGAGTGCACCTCTGCCAAGGTGTGTGGCCGAATGTGAGCAAGTGTCA	2551
QY	2585	CAGGCACTCAGGGATCTTGTGTCCTCCCACTTCTCTGGACTACAAATPAACAATATG	2644
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QY	2645	AATGATATTAATCATCCATCCAGCCACGACGAGGAAAGGAAATTCACTGTAAGGCCGGCAT	2704
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QY	2705	TCGAATCTCCGAAGAGATGTCCTCAAGTTTATGATGGAACMAACACTCCGCGGT	2764
Db	2672	TCAGAGTGTGGAAGAGATCTCTAAAGATATATGATGGAAGAAAGACGTTTCTCACTC	2731
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Db	2732	CAGTGGGACCTTCACTAAATAATACCTTGGGGCTGATCTTAAAGCACAATCCATATC	2791
QY	2825	GTCGTGGCTTGAATTTCAATCATGATCTGAAAAACACAGCAAGGGCTTTGAATGCACT	2884
Db	2792	ACCTGTGCTAAGAGTTCAACCAATGATCTGACACCGACAAGAGTTTCAACTCACT	2851
QY	2885	TTTCAGGTTTGAATCATCAATAATGTAGAGACCCAGGAACCCCAAGTTTGGCTACAGG	2944
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QY	2945	TTCAATGATGAAGTCAATTTTGGCAGGAGCTCGTGTCTTCACTGATGACCTGAGATACA	3004
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QY	3005	GCCGTGGGGATGAGAGAGTCTGTGTCTGATGTGAGAGCGCCGACCTGGGACCGGC	3064
Db	2972	CCATGATAGGAGAACACCTCTGACCTGTTGAATGAGACAGGAGAGTGGGACAAC	3031
QY	3065	CTTGCCCACTGTGTGCGCCGAGTGTGAGAGGACAGTGAAGAGAGAGTGTGGGGCAGG	3124
Db	3032	CACATACCTTGTGATAGCGGAATGTGTGTGATCATGACGCCACATCAGAGAGAA	3091
QY	3125	TGCTGTCAACCCGGGTATCCAGCTCCATATGAACAATCTCAACTGTGATCGACATCG	3184
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Db	3212	ACGACATCTCAAGGTCTGGGACGGGCGGTGACAGTGAACATCTCTGTAAAGAGTGTGA	3271
QY	3305	GTGGCCCGGCCCTGCCAAGGACCTGTGATAGCACTTCAACTCGTGTGCTCGAGTTTCA	3364
Db	3272	GTGGTCCGCCCTTCCGAGAGACATCCACAGCACTTCAACTGACCTCACTCGAGTTTCG	3331
QY	3365	GCACTGACTTTTACACAGCAAGCAGGGCTTTGCAATTTCAATTTTCAAGTGTCCACAGCA	3424
Db	3332	ACAGGACCTTTCATACAGCAAGTCTGGCTTCTTCATATCCAGTTCTCCACCTCAATTGACG	3391
QY	3425	CGTCCGTGAATGACCCCTGGGATCCCGGAGAAATGGGAATGGAGTGTGACAGTTGGGAG	3484
Db	3392	CAACTGTAAAGATCAAGTATGTGCCCAAAATGGCACCCGCTATGAGAGACGACAGAGGG	3451
QY	3485	CCGGGACATTCACAGTGTTCAGATGTACACCTGTGCTACGGCTCCAGGAAAGTGCAGAGA	3544

Db 3452 CTGAGACACCGGTCAATTCACAGTGTACCTGGCTATCAGCTTCAGAGCAAGCAAGCCAAA 3511
Qy 3545 TCAGCTGTGTGAATGAGAAACAGTTCTTCTGAGCAAGCCAGCCCAACATGATCG 3604
Db 3512 TCACCTGTGTGACACTAAATACCGGTTCTTTTGGCAACAGACCCCTCAATGATG 3571
Qy 3605 CTCCCTCGGGGAGACCTGACAGAGCAATCTGGAGCATCCCTCTACCAAAATTACCCAG 3664
Db 3572 CTGCTTGTGAGGGAATCTGACGGGCCAGAGGTGTTATTTGTGTACCCCACTACCCAC 3631
Qy 3665 AACCTAACCCGCGAGGAGAGAGTGTACTGAAAGTACCGTCTGACACAGACTAGCTCA 3724
Db 3632 AGCCGTATCCTCTCGGAGAGGAATGTGACTGAGAGTAAAGGAACCCGAGCTTTGTCA 3691
Qy 3725 TCGCCCTGTATTAATATCTTTAAGCTGAGCTGTGCTATGACTTCTCCATATCTAGC 3784
Db 3692 TCGCTGTGATTTCAAAAGTTTCAACATGAGCCAGCTATGACTTCTTACACATCTATG 3751
Qy 3785 ACGGACGGGACTCTCTCAGCCCTCTCATAGAAAGTTTATGCTCCAGCTCCAGCCG 3844
Db 3752 AAGGGGAAGTTCCACAGCCCTCTCATTTGGAGTTACAGGAGCTTCAAGCCCAAGAA 3811
Qy 3845 GCATTGAAGCAGACAGACAGCTCTTCTCTGCTTCCGACGATGATCTGTAGCA 3904
Db 3812 GAATAGAGTACGCGAAACAGCTGTTCTGCAATTTGAGATGATGCTCGTGCGC 3871
Qy 3905 ATGCTGGCTTCGTATTTGATATACAGAAACCCCGGAGATCATTTTATCTGTT 3964
Db 3872 TTTCAAGGTTTCCGATTTGAATTTAAAGAAACACGGGAGGTTGTTTGAACCAAGAA 3931
Qy 3965 CCATCAAGAACGACACAGGAGTGGGTCGACCTGAAAGTGGGCTCTCCGTCACCTACT 4024
Db 3932 ATATATGAAATGGAGCAAGAGTTGAAACAGACTTCAAGCTTGCATCACATCACTACC 3991
Qy 4025 ACTGCAAGGGGCTACGAAGTTGAGGCACTTCCGACCTGAGCTGATCTGGGAGCTG 4084
Db 3992 AGTGTACTCTGGCTATTAAGATTTCTGACCCCTCATCTCATCTGTGTGATGGGAGCTG 4051
Qy 4085 ATGGGAAGCCCGTGTGAACAATCCCGGCACTGTGCAAGCCCTCGTGGGAGCAAGT 4144
Db 4052 ATGGGAACCTCTCTGGAGCAAGTCTGCTCTGCAATGCTCTCTGTGGAGGCAAGT 4111
Qy 4145 ATGTGGTTTGGAGAGTGTCTGTCTCCCACTACCCCGAAGTCAACAGTGAAC 4204
Db 4112 ACACGGGATCAGAAAGGAGTGTGTTATCAACAACTACCCCATATTAACAGTGTGTC 4171
Qy 4205 AATCTGCTTGTATTTTGTACTGTGCCCAGAGACTATGTGTGTTGGCCAGTTGCTT 4264
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Qy 4265 TCTTTCAACGGGCTCAACGACGTGTGAGGTTCAAGAGCGGCAACAGCACTGCG 4324
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Qy 4325 GCGTCTCACTGCTCTCTGCGGCTCCATACAGAGAACTACTGCTTGGCACTTCA 4384
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Qy 4445 TCTAACAGCGGTTCTCGAACACAGCGCAGCAGTGCAGCTGTGTGCGGAGCCCGCT 4504
Db 4412 TGTATCAAGCTGTTCTCTGTAACAGTACACCCATGAGCTGTCTCCGAGCCCAAGT 4471
Qy 4505 ATGGCAAGAGGCTGGGCACTGACTTCTGTGGGGGCAATGCTGCTTGCATGCAACT 4564
Db 4472 ACGGAAGAGATTTGTCTGTGTTTCTGCGGCTCATGCTGATTCAGATGCAACC 4531
Qy 4565 CCGGCTATGCTCTGAGGGGTGCAAGAGATGAGTGTCTCTGTGCTGGGAGCTTGG 4624
Db 4532 CCGGATACCTGCTTCAAGGTTTCCAGGCGCTTCCACTGCAAGTCCGTGCCAACGCTTGG 4591
Qy 4625 CCCAATGGAATGTCTCAGCGCCACAGTGTGTGTCGCTGTGAGAGCAACCTCAGAGC 4684
Db 4592 CACAGTGAAGCAACAGATCCCAAGCTGTGTGTATCCCTGCAGTGGCAATTTCACTCAAC 4651
Qy 4685 CGAGGGGCAACCTCTGTCTCCCTGTGCTTCCAGAGCCGTACCTCAACGCTCAACTGTG 4744
Db 4652 GAAAGGATCAATCTGTGCTCCCGCTACCTGTAGCCATACGAAACAACTTGAACGTGA 4711
Qy 4745 TGTGAAGATGTGTGCTCCGGAAGCGTGCATCCGATCCAACTGTCTGATTTTGA 4804
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Qy 4805 CAGACAGAACTGGGACTCTGCTGGAAGTATTTGATGTGTCAGATTAACACTGAACATGC 4864
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Qy 4865 TGGGAGTTTCTCAGAAACAACGCTGCTGCTCTTCTGAACAGCACTTCCAAAGCTCT 4924
Db 4832 TGGAAAGCTTCTCAGGACCAACAGTACCGGCACTGTGAACAGTATTTCCAAACCACTCT 4891
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Db 4892 ACTGCAATTTCCAGTCTGACATTTAGTGTGAGCTGCTGCTGTTTCCACTGGAATACAAA 4951
Qy 4985 CGTGGGCTTGAGAGATTGTCCGAACTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5044
Db 4952 CTGTAGGCTTGTGATGTCAGAACACAGACAGCCCTCCCAAGAACAGATCAAAATCGAG 5011
Qy 5045 AGCGCTACTGGTGAATGATGTGTGCTTCTTCCAGTGTGAGCCGGGATATGCTTCCAG 5104
Db 5012 ATCGATCATGTGTGAAGAGCTGTCTTCTTCCAGTGTGAGCCGGGATACCTGTGAGG 5071
Qy 5105 GCCACGCCCATCTCTCTGATGCTCCGGAACAGTGTGGGAGTGAATCACTCTCTCAC 5164
Db 5072 GCCGTTCCACATTTCTGTATGTGACAGGAGCCGTGCTTGGAACTATCCGCTCCC 5131
Qy 5165 TCTGTATTGCACTGTGTGGGGAACAGTGAAGAGATGAGGGGAGTATCTGAGCCCG 5224
Db 5132 TGTGATTTGACACCTGTGAGAGGAGCTGAGCACTTGGGAGTGTGATCTGAGCCCG 5191
Qy 5225 GCTTCCAGGCACTACCCAGTAACATGAGCTGCTCTGGAATAAGCACTGCCGTG 5284
Db 5192 GCTTCCAGGTTCTTACCCCAACATTAAGTACCTGAGAGATCTCTATCCATG 5251
Qy 5285 GCTTGGAGTCAATCAGTCTCTGAACTTCTTCAACGAGCCCAACAGACTACATAG 5344
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Qy 5345 AATTCGGAAATGGCCCTATGAGAACAGCCGATGATGGGAAGTTCAGTGAAGCAGC 5404
Db 5312 AATTTCAAAATGAGCTTACACACAGCCCAATGATGGAACAATTTAGGGGACGAGATC 5371
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Db 5372 TCCCGCGGCTCTGTGAGAGCAACGATGAACCTCTATCACTTTTATAGTACCAT 5431
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Db 5432 CGCAAAACCGGACAGATTTAACTTGTTCACAGCTATGAAATTAAGAACTGTCCAG 5491
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Db 5492 ATCCACCCCATTTCAAGATGGGTATCATATCAATCGAATTAACAGCTGGGGCAATCAG 5551
Qy 5585 TGACTTGTAGTGTCTCCCGGGATATCAATGACTGGCAACCTGTGCTCACTGTCAAC 5644
Db 5552 TATCTTTCAGAGTATATCTGTGGTACATTTATAGGCACTGTGCTCACTGTCAAC 5611
Qy 5645 ATGGCAACAACGGAATGGGAACACCCCTGCGCAAGTGAAGTCCCTTGTGGCGGAG 5704
Db 5612 ATGGGATCAACAGAACTGAATCACTTCTTCAAGATGATGATGCCCTTGTGGGTACA 5671

Qy	5705	ACATCACTCTTCACACGGCACTGGTAATCCCCGGGGTTCCCTAGCCCGATCAAGCT	5764
Db	5672	ACGTAACTCTTCAGAAAGGACCAATCTACTCCCCGGCTTTCGTATGATTCGATCC	5731
Qy	5765	CCCAAGATCTGTCTCTGGCTGATCAACCGTCCCATTTGGCCATGGCGTCCGGCTCAACTCA	5824
Db	5732	TGAAGGAATGCAATTTGGCTCTCAACGAGGCTCCACAGGGACGGAGTTTAACTCAACTTCA	5791
Qy	5825	GCTCTGCTCAGACAGAGCCCTCTGGAGATTTCATATCAATCTGGGATAGGGCCACAGCAA	5884
Db	5792	CCCTGTTTACAGACGGAAAGCTGCAACGATTAATTTGCTTTTGGGACGGTCCCGATCAGA	5851
Qy	5885	CAGACCAACGGCTCGGCTCTTTCACCCGGAGCATAGCCCAAGAAAACATGTGAGATTAT	5944
Db	5852	ACTCAACCCCACTGGAGATTTCATGTGGCAACACAGCCCTCGAAACGGCGATATGCTTCA	5911
Qy	5945	CCAAACCAAGTCTGTCTCAAGTTTCCACCGTGTATGACAGCCACAGGGGGGATCTTCGCCATAG	6004
Db	5912	CCAACCAAGTCTGTCTCAAGTTTCCACAGCGACTTTTCAATATGAGAGGCTTTTGGCTCA	5971
Qy	6005	CTTCTCCGCTTA	6017
Db	5972	ATTTCACGGTCA	5984

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RESULT 7
US-10-276-934-1
: Sequence 1, Application US/10276934
: Publication No. US20030180750A1
: GENERAL INFORMATION:
: APPLICANT: Universlty of leeds
: APPLICANT: Martham, Alexander F.
: APPLICANT: Jackson, Andrew P.
: APPLICANT: Woods, Christopher G.
: TITLE OF INVENTION: Treatment of Cancer and Neurological Diseases
: FILE REFERENCE: 9052-144
: CURRENT APPLICATION NUMBER: US/10/276,934
: CURRENT FILING DATE: 2002-11-20
: PRIOR APPLICATION NUMBER: PCT/GB01/02240
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: PRIOR APPLICATION NUMBER: GB0012186.3
: PRIOR FILING DATE: 2000-05-20
: NUMBER OF SEQ ID NOS: 16
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 1
: LENGTH: 5598
: TYPE: DNA
: ORGANISM: Homo sapiens
US-10-276-934-1

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	Query Match	24.7%	Score 2503.6	DB 15	Length 5598
	Similarity	67.0%	Pred. No. 0	Mismatches 1714	Indels 84
	Matches 3646	Conservative	0	Gaps 3	
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DB	236	TGAG	CCAGAGAGGTGTTCATTTGCTCTG	ACATGTGTCCAGATCTTGGATTCCAGAAA 295	
QY	245	GGGG	CAAAAGACTYAGGCTTCGATTT	CAGTTAGATCCAGCGTCCAGTTCACTTCGAAACG 304	
DB	296	ATGG	TAGAAAGACAGAGTTCCGACITTC	CAAGGTTGGTGCAAATGTACAGTTTCATCTGTGACG 355	
QY	305	AGGG	CTATGACCTGCGAAGGATCC	AGGAGATCACTGTATGAAATGAGCGCATGTTG 364	
DB	356	ACAT	TTCAGTGTCCAGGAGATTTAA	AGCATATCACTGTGCAGAGATTTACAGAGACCTCG 415	
QY	365	CGG	CGCTGAGCGCACACAGGCGAGTCTG	CCGAGCCCGCATGTGTATGATCCCACTTTCGAC 424	
DB	416	CTG	CTTGAAGTAGACACAGGCGCCATCTG	CCGAGCGCAAGAAATGTGATCCCATCTGCGGTG 475	
QY	425	GCCCT	GGGCAATATCACTTCCCCCATTTTCC	CAATTCAGTATGACAAACATGACACT 484	

Db	476	GGCCACAGGGGGTCATTACCTCCCTAAATTATCCGGTTCAGTATGAAATATATGACACT	535
OY	485	GTGTGTGGATATATCAAGCACTCAACCCCTCCAAAGGTGATCAAGCTGCCTTTGAGAGT	544
Db	536	GTGTGTGGGTATACCAACCAACCCGAGCAAGAGTTCATCAAGCTTCCTTTGAAAGGT	595
OY	545	TTGATTTGGAGAGGGGCTATGACACCCCTGACGGTCGGGATGAGTGTGAGGATGGAGAC	604
Db	596	TTGAGCTGAGACGAGGCTATATACACCTTGACGGTTGGTAGTCTGAGAAAGGTGGAGACA	655
OY	605	AGAAAGACGTTCTCTACATGTCTCAAAATGCGTSCAGTGAACAGCCCTTCACACCCAGGCT	664
Db	656	CCAGATGGGTCTTGACGTG-CTACCGGGATTCAGTGTCTTGACCTCA-----T	704
OY	665	CTCGCATCCACAGAGACATGTCTGGGGACATCTGAGGACAGAAATGCACTGTACTTGAGA	724
Db	705	TGTGAGCATGAGCAACAGATGTGGCTACATCTCAGTCGGATGATGACATGTGCTCAC	764
OY	725	TCTGTGCGATATTAGAGTTCAATGCAAGGTCAAGTTCAGTGAAGAACTCCAAAGA	784
Db	765	TGGGT-----	769
OY	785	CTTCTAAATGCTGTGAACTTGTGTCTCCTGGGACAGAGATGACAGGGCAGTTGGCGTG	844
Db	770	-----TTAAACTGTTTACCAAGAAATTGAAAGGAGAGGTGTGGCG	811
OY	845	ACCCTGCGATACCTGCATATGAGCGGAGGAGAGGCTCCCGGTTTACCAACGGTGAACAC	904
Db	812	ATCTGTGAAATCCCGGCTATGGAAAGGGAGCGGACAGAGTTTCTCATGAGATACAC	871
OY	905	TCAAGTTGAGTGCACGCGGCTTTGAGCTGTGTGGGACAGAAAGCAATCATGTCCAA	964
Db	872	TCACCTTTGAATGCCCGGCGGCTTTGAGCTGTGTGGGAGAAAGATTATCACCTGTGAC	931
OY	965	AGAAATTAACCAATGCTGCGCTAAGAGCAAGGCTGCGTGTCTCTGCTTCTTCAACTTCA	1024
Db	932	AGAAATTAACCAATGCTGCGCTAAGAGCAAGGCTGCGTGTCTCTGCTTCTTCAACTTCA	991
OY	1025	CCAGCCCGCTGTGGGGTGTCTGTCTTCCCACTACCCAGAGACTATGCAACCACTCC	1084
Db	992	CGGATCATCTGGGATTAATCTGTCTGCCAAATTAATCCAGAGAAATATGGAAACAACATGA	1051
OY	1085	ACTGTGTCTGCTCATCTGTGCCACAGGCTTGAGACCGCATCACCCTGACCTTCAACACA	1144
Db	1052	ACTGTGTCTGCTTATTAATCTGTGCCAGGAGAAATGCAATCACTAATCTTTATGATTT	1111
OY	1145	TTGAGGTGAGACCTCAGTTTGAATTTCTGTGTCAATCAAGATGGGGCCACGCGACAGCGC	1204
Db	1112	TTGAGGTGAGACCTCAGTTTGAATTTCTGTGTCAATCAAGATGGGGCCACGCGACAGCGC	1171
OY	1205	CCGTCTGTGGGACCTTCTCAGAGAAACAGCTTCCCTCTCCATCAACAAGCATGTGGCCAG	1264
Db	1172	CTGTCTGTGGGACCTTCTCAGAGAAACAGCTTCCCTCTCCATCAACAAGCATGTGGCCAG	1231
OY	1265	TGGCCCGCTCTGAGTTCCAGCTGACCACTCCACAGGAGAGGGGCTTCAACATCACTT	1324
Db	1232	TAGTTCCCTTGAATTTCACTGTACCAATTCCTACTGTGACAGAGGGTTCACATCACTT	1291
OY	1325	TTTACCACTTCCGACACAGAGAGGCCCGATCTCTGGCGTTCCAGTAATGCGAAACGGT	1384
Db	1292	ACACCACTTGTGGTCAAGATGAGGCCATGATCTGTGGCATTCCTATTAACGAGACGACGT	1351
OY	1385	TTGGGAGACAGCTCCAGCTGTGGGACGCTCAATCTCTCTCTGTGATGAAAGGCTTCCCTG	1444
Db	1352	TTGGTGAACAGTTTCTACTCGGAGGCTCGGTTTCTTCCACTGTGATGATGCTTTGTGCA	1411
OY	1445	GGACTCAAGGCTCAGAGACATCACTCTGCGTCTTGAAGAGGGGAGCGTGTCTTGAACA	1504
Db	1412	AGACCCAGAGGATCCGAGTTCATTAATCTGACATACGCAAGACGGGAAAGTGTCTGAGCT	1471
OY	1505	GGCGTGTGCTGGGTGAAAGCTCCCTGTGTGTGACCTGACATTTCCGCCACGCGGACACA	1564
Db	1472	CCACCTGTGCTGGGTGAAAGCTCAATGTGTGACATCTGACAGCGTTCACGCGGAGTCA	1531

QY 1565 TCTCTCTCCGGGCTGGCTGGCTTCTCAAGAGATGCTTGAAGCTGTCCTGGGTGATG 1624
DB 1532 TTTTGGCTCTCCGATGAGCGAGATATATTAAGATTTCTTACATTTGTAATGATATG 1591
QY 1625 AGGCGCCAGCGAGCTACCCCATCAAAATCACTTTCAGAGATTCAAAACCGAGTCAACT 1684
DB 1592 AAGCAAAACAGCGCAGCTCTATCAAAATTAACCTTTTGACAGATTTCAGACAGAGTCAATT 1651
QY 1685 ATGACACCTCGGAAGTACGAGATGGGCGGAGCTTAAGAGCCCTTGAATGGGGTTTACC 1744
DB 1652 ATGACACTTGGAGGTACAGATAGGCGCAGAGTGTGCTCCACTGATGGGAGTACC 1711
QY 1745 ACGGAGCCAGAGTTCCCAAGTCTCTATCAGACACAGCACTAATCTTACCTCTCTCT 1804
DB 1712 ACGGAGCCAGAGCCCAAGTCTCTATCAGACCCGGGAGCTTCAATGACTCTCTATCA 1771
QY 1805 CTACCGACAGAGTCACTCGGACATCGGCTTCCAGCTCCGCTATGAGACTATTAACCTGC 1864
DB 1772 CCACTGCAACAGCGCTCCAGCATCGGCTTCTCTATCCACTATGAGAGTGAACGCTTG 1831
QY 1865 AGTCAGACCACTGCTGATCCAGAAATCCAGTAATGAGACGCGTCATGGGAATGACT 1924
DB 1832 AGTCGATTTCTGCTGATGACCCGGGCAATCCCTTGAACGCGCATTCGCAACGGTGGAGCT 1891
QY 1925 TCTACGTGGGCGCGCTGGTGAACCTTCACTGATGACTCGGCTACACATTAAGTACGGG 1984
DB 1892 TTGGCATCAGGTCCACAGTACTTTCACTGCTGACCCGGGGTACACATTAAGTACGAG 1951
QY 1985 AGCCTCGAGTGTGAGCCCACTTCAAGTGAACCGGCGCTCCGCAAGTTGTAAGCTC 2044
DB 1952 AGCCCTCTGCTGTGAGAGAACACACAGTGAACACGCTTGGCCCACTCGACGCTC 2011
QY 2045 TCTGTGTGGCTTCAATTAAGCTCAAGTGGGACATCTTGTGCGCAGAGGTTCCCTGACT 2104
DB 2012 TATGTGAAGCTATCAAGGGAAGTGGAAACATCTTCTCTGGGTTTCCAGATT 2071
QY 2105 TCTACCCCAACAATGAACTGACCTGATTAATGAAACATCTCAATGCAAGGTTGT 2164
DB 2072 TTTATCAAACTCTTAACGTGACGTGACATGAACTGTCTCATGGAAGAGTTTC 2131
QY 2165 TCTTCACTTTCACACCTTCAACCTGAAATGGGCACTAACCTCCCTCAATCACTGAGA 2224
DB 2132 AATGATCTTTTCAACCTTTCACTTGAAGATTTCCACAGACTTATTAATCAAGAGG 2191
QY 2225 AAGGACGTTTCAACCCAGCCCTTGAAGCACTAACTGATCTGGCTGCGACGCTCCATCA 2284
DB 2192 ATGGAAGTTTTCGAGCCGTTGCAAGGCTCACCGGATCGGTGTGCTCATACAGATCA 2251
QY 2285 GGGCTGGGCTTATGGCACTTCACTGCGCCAGGTCCGCTTCACTGTGATTTTCTCATGT 2344
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QY 2345 CATATGAAGATTCAACATCACTTCTCAGATAGCACTTGAAGCCCTGTGAGAGGCCG 2404
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DB 2372 GAGTCCCTGCTTACGCGGAATGTTGTTTCACTTGTGTGGAGACCTCTGAGCT 2431
QY 2465 TCTCTGCTTCCCGGGTACGCTTGAAGGGGACCGCCGATCACTGTGCTTGGGGGCA 2524
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QY 2525 GACGCGCCTGTGAGCTCGCTTGCAGAGGTGTGTGCTGAGTGGGAATTCACTCA 2584
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DB 2612 AAGTATCATATAAATAGAAACAGAAAGCCGCAAGGCGATCCACTTGAACACAGAGCT 2671
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DB 2672 TCCAGCTGTTTGAAGGAATACTTAAGGTATATGATGAAAGACAGTTCTCTACGTC 2731
QY 2765 TGCTGGAGTTTATGACCATCTGATGATGAGGGGTGACTTTGAACAGCAATTCAGCA 2824
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DB 3152 AAGCAGACCCAGAAACATTAAGCTTCAATTTATTTTTCAGACGGAATGAGCTC 3211
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QY 3545 TCACTGTGTGAAGATGAGAACAGGTTTCTGAGAGCCAGCCGCAACATGATCG 3604
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QY 3725 TGCCCTGTATTTAATCTTTAACTTGAACCTGAGACCTGCTATGACTTCTCATATCTAG 3784

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Db      3692  TGCCCTGTAATTCAAAGTTTCAACATGAGCCCAAGCTATGACTTCTCATACTATG 3751
Qy      3785  AGGAGAGGACCTCTCAGCCCTCTCATAGGAAGCTTCTATGGCTCCAGCTCCAGGCC 3844
Db      3752  AAGGGAGAGTTCACAGCCCTCATTTGGAGTTACAGAGGCTCTCAGGCCCCAGAA 3811
Qy      3845  GCATTAAGACAGCAGCAGCCTCTCTCCGCTTCCGAGAGTATCTGTAGCA 3904
Db      3812  GAATAGAGATAGCGAAGAACGCTGTTTCTGGCATTTTGGAGTATGCTCCGTGGCC 3871
Qy      3905  ATGCTGCTTCTCATTTGATCTATACAGAAAACCGCGGAGTATGTTTGTATCTGTT 3964
Db      3872  TTTCAAGGTTCCGCAATTTAAAGAAACACGAGGAGCTTGTTTTGAACCAAGAA 3931
Qy      3965  CCATCAAGAACGACACAGGAGTGGGCTCCGACCTGAAGCTGGGCTCTCCGTACTACT 4024
Db      3932  ATATAATGATGGAGACAGAGTTGGAACAGACTTCAAGCTTGGCTCCACATCACTACC 3991
Qy      4025  ACTGCACGAGGAGCTACGAAGTTGAGAGGCACTCGACCTGAGCTGATCTGGGGCTG 4084
Db      3992  AGTGTACTCTGCTTAAAGATTTCTGACCTCTCATCTACCTGTGTGATTTGGGGCTG 4051
Qy      4085  ATGGGAAGCCCTGTGTGAAACATCCCGGCAAGTCTGCAAGCCCTGTGGGAGACAGT 4144
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Qy      4145  ATGTGGGTTTGGACGAGAGTGTCTTGTCCCCCACTACCCCAAGAACTACACAGTGGAC 4204
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Db      4292  GACTTCTAGCTCACTCTGGGCTCTCACTCAGGAGAAACATTTGCTTGGCTTACGTCAA 4351
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Db      4352  ATCAAAATTCGCTCCGATTAAGTCAAGCAAGCGGCTCTTGGCCGAGGCTTCACTTGG 4411
Qy      4445  TCTACCAAGCGGTTCTCTGAAACGAGCGCAAGCAAGTCAAGCTTGTGCGGAAACCCGCT 4504
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Qy      4505  ATGGCAAGAGCTGGGCAAGTGAATCTTCTGGTGGGAGCCATGTGCTTCCGTTGAAATGCACT 4564
Db      4472  ACCGAAGAGAAATGTGTTCTGAGTTTCTGCGGCTTCACTGTCGATTTGAGTGAACCC 4531
Qy      4565  CGGCGATAGCCCTGACAGGAGTCCGCAAGATTCAGAGTCCCTGTGAGCTGGGGCTTGG 4624
Db      4532  CGGGATACCTGCTTCAAGGTTTCAACGAGCTTCACTGCAAGTCCGTCACCAAGCCTTGG 4591
Qy      4625  CCCAATGAAATGTCTGACGCGCCCAAGTGTGAGTGTGAGGCAACCTTCAAGAGC 4684
Db      4592  CACAGTGAAGACAGATCCCAAGCTGTGTGATACCTTGCATGGAATTTTCACTCAAC 4651
Qy      4685  GCAGGAGCACTCTGTGCTTCCCTGCTTCCCAAGCCGTAACCTCAACAGCTCACTGTG 4744
Db      4652  GAAGAGGTACATCTGTGCTTCCCGGCTACCTGAGCATTCGGAACCACTTGAACGTGA 4711
Qy      4745  TGTGAAGATGTGTGCTTCCCGAAGGCTGGCATTCAGATTCAGATTTGTGATTTGTGA 4804
Db      4712  TATGAAGATCATAGTTTACGAGAGGCTCGGGAATTCAGATTCAGATGATGATTTTGCA 4771
Qy      4805  CAGAGAGAACTGGAATCTGCTGGAAGTATTTGATGATGATGATTAACATGTAACATGC 4864

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Db      4772  CGAGAGAACTGGGACTCCCTTGAATCCAGATGATGGGAGTGTGACCGCACCCAGAC 4831
Qy      4865  TGGGAGTTTCTCAGGAACAACCGTGTGCGCTTCTGAAACAGACCTCCACAGCTCT 4924
Db      4832  TGGGAAGCTTCTCAGGACACAGTACCGGCACTGTGAACTACTTCAACCACTCT 4891
Qy      4925  ACCCTATTCTTCACTAGATATCAGCGTATCTGCACTGGCTTCCACTTGAATACAAA 4984
Db      4892  ACCGTGATTTCCAGTGTGACATTAATGTGGAGAGCTGTGTGTTTCCACCTGGAATACAAA 4951
Qy      4985  CGGTGGGCTTGACAGACTGTCCGGAACCTGTGTGCTCCAGTAAACGAGGTGAAGCTGGC 5044
Db      4952  CTGTAGCTTGTGTGATCCAGAACAGACCTCCCGACACACATCAAAATGAGAG 5011
Qy      5045  AGGCTACTTGTGGAATGATGTGTGTCTTTTCCAGTGAACCGGAGTATGCTCCAGG 5104
Db      5012  ATCGATACATGTGGAACGAGTGTCTCTTCCAGTGAACCGGAGTACACCTCGAGG 5071
Qy      5105  GCCAGCCCAATCTCTGATGCTCCGGAACAGTGGCGGATGGAATCACTCTCTCCAC 5164
Db      5072  GCGCTTCCCAATTTCTCTGATGCAAGGACGCTTGGCGTTGAACTATCCGTCTCC 5131
Qy      5165  TGTGATGCAAGTGTGGGGAACAGTGAAGAGATGAAGGGGTGATCTTGAAGCCCG 5224
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Qy      5345  AAATCCGAATGAGCCCTTATGAGACCAAGCGCATGATGGAAGATTCAGTGAAGCGAGC 5404
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Db      5372  TCCCGGAGCTCTGAGACCAACGATGAAACCTTCACTTATTAAGTACATTT 5431
Qy      5465  CCCGAATGAGGAGATTCAGAGTGAAGTCAAGCTTCAAGTCAAGTGGCCAG 5524
Db      5432  CGGAACCGGCAAGATTTAACTTGTACCAAGCTTGAATTAACAGACTGTCCAG 5491
Qy      5525  ACCCAGAGCCCTTGTGCAATGTCATTTGAGGAGCTGGCTTCAACGTTGGCAATGAG 5584
Db      5492  ATCCACCCCATTTGAAATGGGTACATGATCAACTCGATTACAGCTGGGAGCAATCAG 5551
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RESULT 8

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US-10-276-934-4
; Sequence 4, Application US/10276934
; Publication No. US20030180750A1
; GENERAL INFORMATION:
; APPLICANT: University of Leeds
; APPLICANT: Markham, Alexander F.
; APPLICANT: Jackson, Andrew P.
; TITLE OF INVENTION: Treatment of Cancer and Neurological Diseases
; FILE REFERENCE: 9052-144
; CURRENT APPLICATION NUMBER: US/10/276,934
; PRIOR FILING DATE: 2002-11-20
; PRIOR APPLICATION NUMBER: PCT/GB01/02240
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: GB0012186.3
; PRIOR FILING DATE: 2000-05-20
; NUMBER OF SEQ ID NOS: 16

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; ORGANISM: Homo sapiens
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; NAME/KEY: misc_feature
; LOCATION: (588)..(588)
; OTHER INFORMATION: "n" is any nucleotide
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (624)..(624)
; OTHER INFORMATION: "n" is any nucleotide
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (672)..(672)
; OTHER INFORMATION: "n" is any nucleotide
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2265)..(2265)
; OTHER INFORMATION: "n" is any nucleotide
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5641)..(5641)
; OTHER INFORMATION: "n" is any nucleotide
; OS-10-276-934-4

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			Gaps	3
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Db	236	TGAGCCAAAGAGGTGTGTGATTGTGTCTGACATGTGTCTCAGATCTCTGGATTCTCAAAA	295	
Qy	245	GGGGCAAAAGACTAAGCTCTGAGATTTCAAGTTAGATTCAGCGTCCAGTTCACTCGCAACG	304	
Db	296	ATGTGTAAAGAGCAGGTTCCGACTTCAGGGTTGTGTCAAAATGTATCAGTTTCATGTAGG	355	
Qy	305	AGGGCTATGACCTCGCAAGGTCCTCAAGCGGATCCAGTCTATATAAGTAGCGACATGTGTTG	364	
Db	356	ACAATTACGTCTCCAGGATCTAAAGACATCACTGTTCAGAGATTACAGACGCTCG	415	
Qy	365	CGGCTCGAGCGACACACAGGCGCATGTGCGGACCGCGATGTGTATGCAATGCCACTTCGAG	424	
Db	416	CTGCTTGAAGTAGCACACAGGCCCATCTGCGGAGCAAACTGTGTATTCAAATGTGTGTG	475	
Qy	425	GCCCCCTCGGGCATCATCACTCTCCCAATTTCCCATTCAGTATGACAAATGACACT	484	
Db	476	GGGCCAGCGCGCATTAATCTCCCTTAATTAATCCGGTTCAGATGAAGATTAATGACACT	535	
Qy	485	GTGTGTGATTCATCATCAGACACTCAACCCCTCAAGGTGATCAACTGCGCTTTGAGGAGT	544	
Db	536	GTGTGTGGGTCAATCAACACACCGACCGGACAAAGGTATCAAGTTTGCCTTGAAGAGT	595	
Qy	545	TTGATTTGAGAGGGGCTATGACACCTGACGGTGTGATGTGTGTGACAGATGGGACC	604	
Db	596	TTGAGCTGAGCGCAGGCTATGACACCTTACCGTTGATGTGTGAGGAGGTGGAGACA	655	
Qy	605	AGAAGCAGTTCTTACATATGTCTCAAAATGCTGCTGATGACAGCCCTCAACCCCAAGCT	664	
Db	656	CCAGATCGGCTTGTATGTCT-----CAOOGGAT 685		
Qy	665	CTCGCATCCCAAGAGCATGTCTGGGACATCTGGAGCAGAAATGACATGTACTTGAGA	724	
Db	686	CCAGTGTCTTGAACCTCAT--TGTGAGCATGAGCAACCAATGTGTGTACTGTGAGT	742	
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Db	743	CGGATATAGCAATTGGC----- 759		
Qy	785	CTTCTAATCTGTGAACTTTGTGCTCTGGGACAGAGATGAGACAGGCAAGTTGGCGGTG	844	

Db	765	-----TCACCTGGGTTTAAAGCTGTTTACCAAGAAATTGAAGAAAGGAGGTGTGGG	811
OY	845	ACCTTGGCACTACTGCAATATGGCCGGAAGGAAGCTCCCGGTTTACCAACGGTACAC	904
Db	812	ATCCCTGGAAATCCCCCTTAATGGGAAGCGGACGAGAGTTTCTCCATATGAGATAC	871
OY	905	TCAAGTTTGAAGCGAGCCGGCTTTGAGCTGTGTGGACAGAAAGCAATCAATGCGAA	964
Db	872	TCACTTTGAATGCCCGCGGCTTTGAGCTGTGTGGGAGAGATTATCACTGTACGC	931
OY	965	AGAATPAACCAATGTCGGCTAAGAGCCAGCTGGTTCCTGCTTCTTCAACTTCA	102
Db	932	AGAAACAATCAGTGGTCTGGCAACAAGCCAGCTGTATTTTTCATGTTTCTTCACTT	991
OY	1025	CGAGCCCGCTGGGGGTGTGCTGCTCCCACTACCAGAGGACTATAGCAACAACCTCC	108
Db	992	CGGCACTACTTGGGATTTTCTGTACCAATATTCAGAGGAATATGGAAACAATGA	105
OY	1085	ACTGTGTGCTCACTCCGTGGCAGGCTGTAGAGCCGATCCACCTGGCTTCAACGA	114
Db	1052	ACTGTGTCTGGTTGATTTATCTCGAGCCAGGAAGTCAATTCACTTAATCTTTAATG	111
OY	1145	TTGAGCTGGAAGCTTCAATTGATTTCTGTGTCATTAAGATGGGCGCACCGCCGAGCGC	120
Db	1112	TGAATTTGAGCTCAATTTGACTTTCGCGGTCAAGAAATGATGGCAATTTCTGACAT	117
OY	1205	CCGTCCTGGGACCTTCTCAGAAACACAGTCTCCCTCTCCATCCACAAGAGTGCACG	126
Db	1172	CTGTCTTGGGTAATTTTCTGGCAATGAATGCTTCCACAGTGGCCAGCACTGGGCA	123
OY	1245	TGGCCGCTCTGAATTCAGACTGACCACTCCACAGGGAAGGGGCTTCAACATCACTT	132
Db	1232	TAGTTCGCTTGGAAATTCAGTCTGACCAATCCACTGACAGAGGGTTCAAATCACTT	129
OY	1325	TTACACCTTCCGACACACAGAGTCCCGGATTCCTGGGCTTCCAGTAATGGCAACGT	138
Db	1292	ACACCAKATTTGGTCAGAAATAGTGCATGATCTGGCAATTCCTATTAACGAGCACTT	135
OY	1385	TTGGGACAGCTTCCAGCTGGGACCTCACTCTCTTCTCTGTGATGAAGCTTCTT	144
Db	1352	TTGGGACAGGTTTCTACTCGGAGAGCTGGTTCCTTTCACATGATGATGACTTTG	141
OY	1445	GGAATCAGGGCTCAGAGACCAATCACTCCGCTCTGGAAGAGGAGCGCTGTCCGACA	150
Db	1412	AGACCCAGGGATCCGAGTCAATTCCTGCATATCTGCAAGAGGGAACGTGTCTGAACT	147
OY	1505	GCGCTGTCTCCGCTGTGAAGCTCCCTGTGGTGTCACTGACTTGCACAGCGGACCA	156
Db	1472	CCACCGTCCCGGCTGTGAAGCTCATGTGTGGACATCTBACAGCGTCCAGCGGAGTCA	153
OY	1555	TCTCTCTCTCGGGCTGGCTTGGCTTTCAGAGATGCTTGAAGCTGTGCTCTGGTGA	162
Db	1532	TTTGTGCTTCTGGAATGGCCAGAAATTAATAAGATCTTTTTCATTTGGAATGAAT	159
OY	1625	AGGCCAGCCAGGCTACCCCTCAAAATCACTTTCGACAGATTTCAAAACGAGGCTCACT	168
Db	1592	AAGCAAAACAGGCGCACTTATCAAAATTACTTTTGAACAGTTTTCAGACAGGTCAATT	165
OY	1685	ATGACACCTTGAAGTACGCGATGGCGGAACTTACAGCGCCCTTGATCGGGTTTACC	174
Db	1652	ATGACACTTGTGAAGTACAGAGATGGGCGAGCAAGTTGTGCTCCCACTGATCGGCA	171
OY	1745	ACGGGACCCAGGTTCCCAAGTTCTCATACAGACACAGCACTTACTTACTCTCTTCT	180
Db	1712	ACGGGACCCAGGCAACCCAGTTCTCATACAGACACGGGAATTTATGATCTTGTAAT	177
OY	1805	CTACCGACAAGATCACTCGGACATTCGGCTTCCAGTCCGCTATGAGACTTAAACATGC	186
Db	1772	CCACTGACAACAGCGGCTCCAGCATGGGCTTCCATTCACCTATGAGAGTGTACGCT	183
OY	1865	AGTACAGCACTGTCTGATTCAGGAATCCCAATTAATGAACAGCTCATGGGAATGACT	192
Db	1832	AGTGGAAATCTCTGCTTGAACCCCGGCAATCTCTGTGAACGGCAATCGCACGCTGGA	189

OY	1925	TCYAGTGGCGCGCTGGTGAACCTTCACCTGTGAATCGGGCTACACATTAAGTACGGCG	1984
Db	1892	TTGGATCAGGTCCACAGTGAATTTTCACCTGTGAACCGGGGTACACATTAAGTACGACG	1951
OY	1985	AGCCTCTGAGTGTAGGCCCAACTTCAGTGGAGCGGGGCCCTGGCCAGTTGTGAAGCTC	2044
Db	1952	AGCCCTCGTCTGTGAAGAGAACCCAGTGGAACAGCCCTTGGCCAGCTGCCAGCTC	2011
OY	2045	TCGTGTGGCTTCATTCAAGGCTCCAGTGGAGCCATCTGTGGCGCAAGGTTCCCTGACT	2104
Db	2012	TATGTGGAGGCTACATCCAAAGGAAGATGGAAACAGTCTTTCCTCTGGTTCCAGATY	2071
OY	2105	TCYACCCCAACAACTTGAACCTGCACCTGGATTATGAAACATCTCAATGGCAAGGTGTG	2164
Db	2072	TTTATCCAAACTCTTAACCTGCAGGTGACCATTTGAAGTGTCTCATGGAAGAGATTC	2131
OY	2165	TCYTCACCTTCCACACTTTCACCTGGAAGTGGCAGTACCTCTCTCATCTGAGA	2224
Db	2132	AAATGATCTTTCACACTTTTATCATCTTGAAGTTCACAGACTTATTAATGATACAGAG	2191
OY	2225	ACGGCAGCTTCAACCCAGCCCTGAGGACCTTAATCTGATCTTCGGCTGCCAGCTCCATCA	2284
Db	2192	ATGGAAGTTCCTCCAGGCCCGTTCAGAGCTCACCGGGTCGGTGTGCTCATGATCA	2251
OY	2285	GCGCTGGGCTCTATATGGCAACTTCACTGGCCAGGTCCGGTTATCTGTATTTCCATGT	2344
Db	2252	AGCGAGGCTCTGTGGAACCTTCACTGCCAGCTTCGGTTTATATCAGACTTCTCATATT	2311
OY	2345	CATATGAAGATTCAACATCACTTCTCAGAGTACGACTTGGAGCCCTGTGAGGACCCG	2404
Db	2312	CGTACGAGGGCTTCATATATCACTTTTCAGAAATGACTTGGAGCAATGATATCTGT	2371
OY	2405	AGTCCCAAGCCTAACAGCATCCGGAAGGCTTGACGTTGGGTGGCGCACACTTGAAGCT	2464
Db	2372	GAGTCCCTGCTTACCGGAAGATTTGTTTTCATCTTGTGTGGAACTCTCTGAGCT	2431
OY	2465	TCYCTGCTCCCGGGTACCGCTGTGAGGACCCCGCATCACTGCTGGGGGGCA	2524
Db	2432	TTTCTGCTTCTCGGATATGTTTGAAGGTGCACCAAGCTTAAGTCTGGGGTGGGG	2491
OY	2525	GACGGCGCTGTGAGGCTCGCTCTGCCAAGTGTGTGCTGAGTGTGGAATTCAGTCA	2584
Db	2492	GCCGCCGTGTGTGAGTCACTTCGCCAAGGTGTGTGCCGAATGTGTGACCAAGTGTCA	2551
OY	2585	CAGGCACTCAGGGTCTTGTGCTGTGCCCCCACTTCTGTGACATCAATTAACATATG	2644
Db	2552	AAGGAATGAAGAACATTACTGTCTCCAAATTTTCCATTCMAATTATATTAATCAATG	2611
OY	2645	AATGCATCTACTCCATCCAGACCAGCAGGGAAGGAATTCAGCTGAACCCAGGGCAT	2704
Db	2612	AGTGTATCTATAAATATGAACACAGAACGGGCAAGGGCATCACCTTGAGACAGAGCT	2671
OY	2705	TCGAACCTCCGAAGGAATGTCTCAAGTTTATGATGGAACAACAACCTCCGCCGT	2764
Db	2672	TCAGACTTGTGAAGGAATACTCTAAAGGTATATGATGAAAAAGACAGTTCTCTCAGTC	2731
OY	2765	TGCTGGGAGTTTGTAGCAATCTGAGATGTGGGGGTACTTTGAAACGACATCCAGCA	2824
Db	2732	CACGTGGACGTTCACTTAAATATGAACCTTGTGGGGCTGATCTTAACGACATCTCAATC	2791
OY	2825	GTCGTGGCTGTATTTCACTACTGATGTGAAAAACACAGCAAGGGCTTTGAATGCACT	2884
Db	2792	ACCTGTGCTGTAGTTTCAACACCAATGATCTGACACCGAACCAAGTTTCACTCACT	2851
OY	2885	TTTCAGCTTGAACCTCATCAAAATGTGAGACCCAGAAACCCCAAGTTTGGCTTACAGG	2944
Db	2852	ATACCAAGTTTGTATCTGGTAAATGTGAGATCCGGGCAATCTCTTAATCAGGCTATAGGA	2911
OY	2945	TTTCATGATGAAGTCAATTTTGCAGGAGCTCGTGTCTCTTCACTGTGACCTTGGATACA	3004
Db	2912	TCCGTGATGAAGGCACATTACCGCACTGTATGTTCTTAAGTTGCAACCCGGGGTAGC	2971

QY	3005	GCCTGCGGGGATGATGAGAGCTGCTGTGTCTGATGTGAGAGACCGCCGACCTCGGACCCGGC	3064
Db	2972	CCATGTCATGGAGCAACAACCTTGACCTGTGTTGATGTGAGACAGAGAGTGTGGACAAC	3031
QY	3065	CTGTCGCCACCTGTGTGCGCGAGTGTGGAGGGACAGTGAAGAGAGAGTGTGCGGGCAGG	3124
Db	3032	CACATCCTTCTGTGCATACCGGAATGTGTGTCTAGATTCATGACGCCACATCAGAACGA	3091
QY	3125	TGCTGTACCCCGGGATATCACTGCTCCCTATGAAACAATCTTCACCTGATCTGACCAATCG	3184
Db	3092	TATGTGTCCCTGTGGTATCACTGACCTCGATATGACAAACCTCACACTGCACCTGGATTATAG	3151
QY	3185	AAGCAGAGGGCCGGCTGCACCAATTGGGGCTACCTTCTGTGTGTTGACACAGAGAGTTCC	3244
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QY	3245	ACGACGTGCTGGCATCTGGGATATGGGCTGTGGAGACGGGGCTCTGTGTAAGAGCTGA	3304
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QY	3305	GTGGCCCGGCGCTGCCCAAGAGACCTGTACATAGACCTTCAACTCGTGTGCTCGTCACTTCA	3364
Db	3272	GTGGTCCGGCCTTCCGAGAGACATCCACAGCACCTTCACTCACTCACTCGAGTTCC	3331
QY	3365	GCATGACTTCTTCAACGACAGAGAGGGCTTTGCCATTCAAATTTTCAGTGTCCACAGCAA	3424
Db	3332	ACAGGACATTTCTTATCAGCAAGTCTGGCTTCTCCATTCAGTTCTCCACCTCAATTCAG	3391
QY	3425	CGTCTTGAAATGACCTCTGGGATCCCCGAGAAATGGGAATCGGAGTGTGACAGTTGGGAG	3484
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QY	3485	CCGGGCACTCCACAGTGTTCAGTGTGACCTGTGCTACGGCTCAGGGAAAGTCAAGA	3544
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QY	3545	TCAGCTGTGTAAGATCGAAGAACAGTTCCTCTGGACGCCCAAGCCGCAACATGATCG	3604
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Db 5252 GCTATGTGACATATTTAGTTTCTGAAATTTTCTTACGAAAGCTATATGATGATGAT 5311
Qy 5345 AAATCCGAATGCGCCCTATGAGACAGCGCATGATGGAAGATTCAGTGAAGCGAGC 5404
Db 5312 AAATCAAAATGAGACTTACACACAGCCCATGATTTGACATTTAGCGGCAAGATC 5371
Qy 5405 TTCCAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 5464
Db 5372 TCCCGCGGCGCTGTGTGAGCAACAGCATGAAACCTCATCTTATGATGACAT 5431
Qy 5465 CCAGAAATCGGCGCAGATTCAGCTGAGTATCAGGCGCTA 5504
Db 5432 CGCAAAACCGGCAAGATTTAACTTGAAGCTTACCAAGCTTA 5471

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RESULT 9
US-10-276-934-2
; Sequence 2, Application US/10276934
; Publication No. US20030180750A1
; GENERAL INFORMATION:
; APPLICANT: Universlity of Leeds
; APPLICANT: Markham, Alexander F.
; APPLICANT: Jackson, Andrew P.
; APPLICANT: Woods, Christopher G.
; TITLE OF INVENTION: Treatment of Cancer and Neurological Diseases
; FILE REFERENCE: 9052-144
; CURRENT APPLICATION NUMBER: US/10/276, 934
; PRIOR FILING DATE: 2002-11-20
; PRIOR APPLICATION NUMBER: PCT/GB01/02240
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: GB0012186.3
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 6145
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (588)..(588)
; OTHER INFORMATION: "n" is any nucleotide
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; LOCATION: (624)..(624)
; OTHER INFORMATION: "n" is any nucleotide
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; OTHER INFORMATION: "n" is any nucleotide
; NAME/KEY: misc feature
; LOCATION: (6027)..(6027)
; OTHER INFORMATION: "n" is any nucleotide
US-10-276-934-2
Query Match 24.2%; Score 2450.2; DB 15; Length 6145;

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Best Local Similarity 66.9%; Pred. No. 0;
Matches 3568; Conservative 0; Mismatches 1678; Indels 84; Gaps 3;

QY	185	TTAACTCAGGTTGGTGTGTCCTCAAGGACATATATATGTGTCAGACCCCTGGCATACCCGAAA	244
Db	236	TGAGCCAGAGAGGTGTGCTATTGGTCTTGACATGTGTGTCAGATCTGGGATTTCCAGAAA	295
QY	245	GGGGCAAAAGCTAGGCTCGGATTTTCAGGTTAGATTCAGCGGTCCAGTTCACTTGCACACG	304
Db	296	ATGGTAGAAGACAGGTTCCGACTTCAGGGTTGGTGCAAAATGTACAGTTTTCATGTGACG	355
QY	305	AGGGCTATGACCTGCAAGGGTTCCAAGCGGATTCACCTGTATGAAAGTAGCGACATGTTTG	364
Db	356	ACAAATTAGTCTCCAGGGATCTAAAGACATCACCTGTCAAGAGTTTCAAGACAGCGCTCG	415
QY	365	CGGCTGGAGGACCAACAGGCGAGCTGTGCGAGCCCGCATGTGTGATGATGCGCACCTTGAG	424
Db	416	CTGCTTGAAGTGAACCAAGGCCCATCTGTCCGAGCGAAGACATGTGATATCAATCTTGCGTG	475
QY	425	GCCCCCTGGGATCATCACTCTCCCAATTTTCCCATTCAGTATGACAAACATGACACACT	484
Db	476	GGCCACAGGGGTCTATTACTCTCCCTAATTATCCGGTTCAAGTAGAAGATATGACACT	535
QY	485	GTGTGTGATCATCAACAGACTCAACCCCTCCAGGTATCATAGCTCGCCTTTGAGAGT	544
Db	536	GTGTGTGGGTATCAACCAACCGCACCGGCAAGGTATCAAGCTTGCTCTTNGAAGGT	595
QY	545	TTGATTTTGGAAGGGGCTATGACACCCGTAGAGGTGGGTGATGTGTGATGAGATGGGAGCC	604
Db	596	TTGAGCTGGAACGAGGCTATGACACCTTCAGGTGTGTGATGCTGGAGAGGTGGAGACA	655
QY	605	AGAAAGACAGTTCTCTACATGTCTCAAAATGCTCGATGACAGACCCCTCACACCCAGGCT	664
Db	656	CCAGATCGGTCTTGTANGTGCT-----CAACGGAT	685
QY	665	CTCGATCTCCAGAGACATGTCTGGGACATCTGAGGCAAGAAATGACTGTACTTGAGA	724
Db	686	CCAGGTCTCCGACCTCAT--TGTGACATAGAGCAACAAATGTGGCTAGATCTGCAGT	742
QY	725	TCTGTGCGGACATTAGACGTTCAAGTGAAGGTCAAGTTCAGTAGAGAAAGTCCCAAGA	784
Db	743	CGAATGATAGCATTTGGC-----	759
QY	785	CTTCTAATGCTGTGGAACTTGTGTCTCTGGGACAGAGATGAGCAGGCGAGTTGGCTGTG	844
Db	760	-----TCACTGGGTTTAAAGCTGTTTACCAAGAAATTGAAAGGGAAGGTGTGTGGG	811
QY	845	ACCCTGCAATCTGCAATATGAGCCGGAGGGAAGGCTCCCGGTTTCAACAAGTGAACAC	904
Db	812	ATCTCGGAATCCCGCTATGGGAAGCGGACGGAGCAAGTTTCTCATGGAAGATACAC	871
QY	905	TCAAGTTGAGATGCCAGGCCCGCTTTGAGCTGTGTGGGACAGAAAGCAATGCATATGCCAA	964
Db	872	TCACCTTGAATGCCCGGCGGCTTTGAGCTGTGTGGGGAAGAGATTTACACTGTGCAC	931
QY	965	AGAAATTAAACAATGTCGGCTAAAGACGAGGCTGTGTTCTCCGCTTTTCAACTTCA	1024
Db	932	AGAACATCAAGTGTCTGGCAACAAGCCACGTGTGATTTTTCATGTTTCTTCAACTTAA	991
QY	1025	CCAGCCGCTGGGGTTGTCTGTCTCCCACTACCCAGAGACTATGGCAACCACTTCC	1084
Db	992	CGGCATCATCTGGGATTTATTTCTGTCAACAAATTATCCAGAGAAATATGGGAAACAACATGA	1051
QY	1085	ACTGTGTGTGCTCATCTGTGGCAGGCTGTGAGAGCGGATCATCCTGGCTTTCAACGACA	1144
Db	1052	ACTGTGTGTGTTGTTATCTGTGAGCCAGGAAGTGCATTTCACTTAATCTTTAATGTAT	1111
QY	1145	TTGACGTGAGAGCTCAGTTTGTATTTCTGTGTATCAAGATGAGGCGCACCGCCGAGCGC	1204
Db	1112	TTGATGTTGAGGCTGAATTTGACTTTCTTCGGGCTCAAGAGATGATGCGACTTTCTGACATA	1171
QY	1205	CCGTCTGGGACCTTCTCAGGAAACAGCTTCCCTCTCATCAACAGCAGTGGCACG	1264

Db	1172	CTGTCCTGGGATCACTTTTCTTGGCAATGAAAGGCTTCCACGCTGGCCAGCAGTGGGCATTA	12311
Qy	1265	TGGCCCGCTCTCGAGTTCCAGACTGACCACTTCCACAGGAAAGAGGGGCTTCAACTCACTT	1324
Db	1232	TAGTTCCCTTGGAAATTTCAAGTCTGACCATTTCCACTGGCAGAGGGTTCAACATCACTT	12911
Qy	1325	TTTACCACTTCCGACACAAGAGAGGCCGGATCCCTGGGGTTCCAGTAAATGGCAAAACGGT	1384
Db	1292	ACACCAATTTGGTCAGAAATGAGGCCATGATCTCTGGCAATTCATATAAACGACAGCGTT	13511
Qy	1385	TTGGGGAACAGCTTCAGACTGGGAGCTCCATCTTCTCTCTGTGATGAAGACTTCCCTTG	1444
Db	1352	TTGGTGAACAGTTTCTACTGGGAGCGTGGTTCTTCCACTGATGATGGCTTTGTCA	14111
Qy	1445	GGACTCAAGGCTCAGAGCAATCACTCTGCGTCTGAAAGAGGGCAGCGTGTCTGGAACA	1504
Db	1412	AGACCCAGGGAATCCGAGTCCATTACTGCAATCTGCAAAAGCGGAAAGTGGTCTGAGCT	14711
Qy	1505	GCGGTGCTGCGGCTGGAAGCTCCCTGCTGGTGTCACTGACTTCCGCCAGGGGACCA	1564
Db	1472	CCACCGTGCCCGCTGTGAAGCTCAATGAGTGAATCTGACAGCGTCCAGCGGAGTCA	15311
Qy	1565	TCCCTCTCCGGGCTGGACCTGGCTTCTCAACAAGATGCTTGAAGCTGTGCGCTGTGATTG	1624
Db	1532	TTTTGCTCTCTGGAATGGCCAGGATATATTAAGATTTCTTACATTGTGAATGATATATG	15911
Qy	1625	AGGCCCAGCAGGCTACCCCATCAAAATCACTTTCGACAGATTCAAAACCGAGGTCACT	1684
Db	1592	AAGCAAAACAGGCCACTATCAAAATTAATCTTTGACAGATTTCAACAGAGGTCAATT	16511
Qy	1685	ATGACACCCCTGGAAGTACGCGATGGGGGAGCTTACTAGCGCCCTTGAATGGGGTTTACC	1744
Db	1652	ATGACACTTGTGAAGTCAAGATGGGGCAGCAGTGTGTCCCACTGATCGGCAGATACC	17111
Qy	1745	ACGGGACCCAGGTTCCCAAGTTCTCTCAATGACACACAGCAACTACCTCTACCTCTCTCT	1804
Db	1712	ACGGGACCCAGGACCCCAAGTTCTCTCAATGACACCGGAACTATGATACCTGTATTCA	17711
Qy	1805	CTACCGACAAGAGTCACTCGGACATCGGACTTCCAGCTCCGCTATGAGATATTAACACTGC	1864
Db	1772	CCACTGACCAACAGCCGCTCCAGCATCGGCTTCCCTATCCACTATGAGAGTGTGACGCTTG	18311
Qy	1865	AGTCAAGCACTGTCTGTGATCCAGGAATCCCAATTAATGACAGCGTCTATGGGAATGACT	1924
Db	1832	AGTGGGATTCCTGCTGTGACCCCGGCAATCCCTGTGAACCGGCATTCGCGCAGTGGAGACT	18911
Qy	1925	TTCTACGTGGGCGGCTGTGATCCTTACGCTGTGACTGGGCTACACAATTAAAGTACCGGG	1984
Db	1892	TTGGCATACAGTCCACAGTGACTTACGCTGTGACCCGGGTTACACATTAATGATACAGC	19511
Qy	1985	AGCCTCTGAGTGTGAGCCCAACTTCCAGTGTGAGCCGGGCTCTGCCAGTGTGAAAGCTC	2044
Db	1952	AGCCCCCTGTCTGTGAGAGGAACCAACAATGTGAACACAGCCTTGGCCAGCTGGCAGCTC	20111
Qy	2045	TCTGTGTGCTTCAATTCAAAGCTCCAGTGGGACATCTTGTGGCCAGGGTTCCCTGACT	2104
Db	2012	TATGTGAGGCTACATCCAAAGGAAGTGGAAACAGTCTTTCTCTGGGTTTCCAGATTT	20711
Qy	2105	TTCTACCCCAACAATTGAATCGGACCTGTGATTAATCGAAACAATCTACAGGAAGGTGTGT	2164
Db	2072	TTTATCCAAACTCTCTAACTGACGTTGACATTTGAAGTGTCTCATGGGAAAGAGATTTC	21311
Qy	2165	TCTTCACCTTTCACACCTTCCACCTGGAAGTGGCCATGACTACCTCTCTCACTGAGAGA	2224
Db	2132	AAATGATCTTTCACACCTTTCATTTTGAAGTTCCCAAGACTAATTTACTGATATCACAGAG	21911
Qy	2225	ACGGCAGCTTCAACCAGCCCCCTGAGGAGCTTAATGTGATCTCGGCTGCGCAGCTCCCATCA	2284
Db	2192	ATGGAAGTTTTTCCGAGCCCGTGTCCAGAGCTCACCGGATCGATGTTCCTCATATCATCA	22511
Qy	2285	GCGCTGGGCTCTAATGCAATTCATCTGCCAGGTCGCGCTTCACTCTGATTTTCTCCATGT	2344
Db	2252	AGGCAAGGCTGTGGAATCTTCACTGCGCCAGCTTGGTTGATTAATACAGACTTCTCAATTT	23111

QY	2345	CATATGAAGATTTCACATCACTTCTCAGAGTATGCACTCTGGAGCCCTGTGAGAGCCCG	2404
Db	2312	CGTACGAGGGGCTTCAMATTCACATTTTCAGAAATATACCTGGAGCCATGTGATCTGTG	2371
QY	2405	AGGTCACGAGCTTACAGCATCCGGAAGGGCTGTGAGTTGGGTGGGGCCACACTTGA	2464
Db	2372	GAGTCCCTGGCTTCAGCCGAAAGATTTGGTTTTCATCTTGTGTGGAGACTCTTCGACGT	2431
QY	2465	TCCTCTGCTTCCCGGGATCCGTCTGGAGGGACCGCCGCATCAAGTCCCTGGGGGCA	2534
Db	2432	TTTCTCTGCTTCCGGGATATCTGTTTGAAGGTGGCCACCAAGCTTACCTGCGGGTGGG	2491
QY	2525	GAGGGGCGCTGTGGAGCTGGCCTCTGGCCAAAGGTGTGTTGTAAGTGTGGAAATTCAGTCA	2584
Db	2492	GCGGCGGTGTGTGAATGACCTCTGCAAGGTGTGTGGCCGAATGTGAGCAAGTGTCA	2551
QY	2585	CAGGCACTCAGGGTACTTTGCTGTCCCGCCACTTTCTGTGAACTTACATTAACATATG	2644
Db	2552	AAGGAATGAGAGGAATTAAGTCTCCAAATTTTTCATCCAAATTAATTAATTAACATG	2611
QY	2645	AATGCATCTAATCTCCATCCAGACCCAGCCAGGGAAGGAATTCAGTGAAGCCAGGGCAT	2704
Db	2612	AGTGAATCTATAAATAAGAAAGAGCCGGGCAAGGGATCCACTTGAACAAGAGCT	2671
QY	2705	TCGAATCTCCGAGAGAGATGTCTCAAGTTATGATGGGCAACAACAATCCGGCCGTT	2764
Db	2672	TCCAGCTGTTTGAGAGGATTAATCTTAAGGTATATAGTGAAGAAACAGTTCCTACAGTC	2731
QY	2765	TGCTGGGAATTTTGAACCATTTCTGAGATGATGGGGGTGACTTTGAACGACATCCAGCA	2824
Db	2732	CAGTGGGCAAGTTTCACTTAATAATGAACTCTGGGGCTGATCTTAAGACGACATCCAA	2791
QY	2825	GTCTGTGCTTATTTTCATCACTGATGCTGTAAGAAACACGAGAAGGGCTTGAATGAC	2884
Db	2792	ACCTGTGGTAAAGTTTCAACACCAATGATCTGACACCGACCAAGTTTTCATCACT	2851
QY	2885	TTTCCAGCTTTGAATCATCAAAATGTAGAGCCAGAACCCCAAGTTTGGCTACAGG	2944
Db	2852	ATACAGATTGATCTGTGTAATAATGTAGAGATCCGGGATCTCTTAACAGGGCTATAG	2911
QY	2945	TTTCATGATGAAGTCATTTTGGAGGAGACTCCGTGCTCTTCAAGTGTGACCTCGATACA	3004
Db	2912	TCCGTGATGAAAGCCACTTTTACCAACTGATGTTCTGTACAGTTTGAACCCGGGGTACG	2971
QY	3005	GCTTGGGGGTATGTAGAGAGCTGCTGTGTCGTAGTGTGAGAGCGCCGACCTGGGACCG	3064
Db	2972	CCATCATATGGCAACAACCTGACCTGTGATGTGAGTGGACAGAGAGATGTGGGACAA	3031
QY	3065	CTTGTCCCAACCTGTGTGGCCGAGTGTGAGGGAACATGAGAGAGAGAGTCCGGGCAAG	3124
Db	3032	CACATACCTTGTGTGATAGCGGAATGTGTGTGATGATCAATGACAGCCACATTCAGACGA	3091
QY	3125	TGCTGTACACCGGGTATCCAGCTCCATATGAAACAATCTCAACTGTATGTGACCATCG	3184
Db	3092	TATTTGCCCTGTGATATCCAGCTCCGATATGACAAACCTCCACTGCACCTGGATTATATG	3151
QY	3185	AAGCAGAGGCGGCTGTGACCATTTGGGCTACATTTCTGTGTGTTGAACAAGAGAGTTTC	3244
Db	3152	AGGCAGACCCAGGAAAGCACTTAAGCTTCATTTGTTTTCGACACGGAGATGGCTTC	3211
QY	3245	ACGAGTGTCTCCGATCTGGGATGGGCTGTGAGAGACCGGGGTTTGTGTGAAGAGCTCA	3304
Db	3212	ACGACATCTCAAGGTCTGGGACGGGCGGTGTGACATGTGATCTTGTGTAAGAGATGGA	3271
QY	3305	GTGGCCGGGCGCTGTGCCAAGGACTTGATAGCACTTGAACCTGGTGTCTGTCAATTTCA	3364
Db	3272	GTGGTCTCGCCCTTCGAGAGCAATTCACAGCACTTCAACTCACTCACCTGTGAGTTG	3331
QY	3365	GCAGTGAATTTTACACAGCAAGAGGGCTTGTGCAATTAATTTTCAAGTGTCAACAGCA	3424
Db	3332	ACAGGCACTTTATATAGCAAGTGTGGCTTCTTCATACCAATTCACCTCAATTTGAG	3391

QY	3425	CGTCTGCATGACCTCGGATATCCCGACAAATGGAGTGGAGTGGATGTGACATTTGGAG	348
Db	3392	CAACCTGTAAAGATCAAGGTATCCCAAAATGTGACCCGCTATATGGAGACAGCAGAGG	345
QY	3485	CCGGGCACTCCACAGTGTTCAGTGTGACCTTGGCTACGGGCTGACAGGGAAATGACAGA	354
Db	3452	CTGGAGACACCGTCACATTCAGTGTGACCTTGGCTATCAGCTCCAAAGAACCCAAAB	351
QY	3545	TCAGCTGTGAAAGATCGAAGACAGGTTCTTCTGGCAGCCCAAGCCCGCAATGCATCG	360
Db	3512	TCACCTGTGTGACGTGAATTAACCGGTTCTTTTGGCAACAGACCTCTCACTGATAG	357
QY	3605	CTCCCTGCGGGGAGACTGACAGACCAATCTGAGTCAATCCCTCAACCAATATACCAG	366
Db	3572	CTGCTGTGTGAGGGAATCTGACGGGCGCAGAGTGTATTTTGTATCCCACTACCAC	363
QY	3665	AACCTTACCCCGCAGGCAAGAGTGTGACTGTGAATAAGTCGCTTCCACAGACTAGTCA	372
Db	3632	AGCCGTATCTCTCGTGGAGGAATGTGACTGGAGATTAAGTAACCGGACTTTGTGA	369
QY	3725	TGCGCTGTGATTTTAACTTAACTTAACTGGAGCTTGGCTATGACTTCTCTCATTTACG	378
Db	3692	TGCGCTGTGATTTTAAATTTCAACATGGAACCCAGCTATGACTTCTTCACTATAG	375
QY	3785	ACGAGCGGACTCTCAAGCCCTCATATGAAAGCTTATGAGTCCCAAGCTTCCAGGCC	384
Db	3752	AAGGGGAAGATTCCAACAGCCCTCATTTGGAGATTAACAGGCTCTCAGGCCCCAGAA	381
QY	3845	GGATTGAAGACGACGACCAAGCTCTTCTGTGCTTCGACGAGATGATTTGTAGCA	390
Db	3812	GAATGAGATGACGGAACACCTGTTCTTGGCAATTCGAGTATGTCTCCGAGGCC	387
QY	3905	ATGTGCTTCTGCTCATTTGACTATAAGAAAAACCCGCGGAGATCATGTTTGAATCTGGT	396
Db	3872	TTTCAGGGGTGGCCATGATTTTAAAGAAACCAAGGAGCTTGTTTGACCCAGAA	393
QY	3965	CCATCAAGACGACACAGGGTGGGCTCGACTGAAGCTGGGCTCTCCGTCACTACT	402
Db	3932	ATATATGATGGGCAAGAGTTGGACACTTCAACTTGGCTCCACATCACTACC	399
QY	4025	ACTGCAAGGGGCTACACAGTGTAGGGCACTGCAACCTGACGTGCATCTCGGGGCTG	408
Db	3992	AGTGTGACTGTGGCTATTAAGATTTCTTGACCCCTCATCCATCACTGTGTGAATGGGGCTG	405
QY	4085	ATGGAGACCCCGTGTGAACAATCCCGGCAAGTGTGCACAGCCCTGTGGGGACAGT	414
Db	4052	ATGGGAAACCTCTCGGGACCAAGTGTGCCCTCTGCAATGTCTCCGTGTGAAGGCACT	411
QY	4145	ATGTGGTTCGAGAGGTGTGCTGTGTCCCACTAACCCCAAGACTACACCACTGAC	420
Db	4112	ACAGGGGATCAGAAAGGTATTTATACCAAACTACCCCATTAATTACACAGCTGTCT	417
QY	4205	AGATCTGCTTATTTTGTATCTGTGACCAAGACTATGTGTGTTTGGCAGTTCGCT	426
Db	4172	AAATATGCTCTATTTTCATCAACGATCAAAAGAAATCTGTGTCTTTGAGACGTTTGCT	423
QY	4265	TCTTTCAACGGCCCTCAACGACGTGTGAAGGTTTCAACAGCGCCACAGCAGACTGCG	432
Db	4232	ATTTCAGACAGCCCTGATGATATTTGGCAGATTAATTGTATGAAACCATTCACAGGCCA	429
QY	4325	GGCTCTCAGTCCCTCTCGGGGCTCCCATACAGGAGATCACTGCTTGGCCACTTCA	438
Db	4292	GACTTTCAGTCACTCTCGGGGTCTACTCAGGGGAAATTTGCCCTTTGGCTACGTCAA	435
QY	4385	ATCAAGTTCTCATTAAGTTCAAGCGCCAAAGGCTTCGACCAAGCCAGAGGCTTCACTTTG	444
Db	4352	ATCAAAATTCGCTCCGATTCAGTGAAGAGAGCGGTGCTCTGCGCGGCTTCACATTCG	441
QY	4445	TCATCAAGAGGCTTCATCAAGACAGGCGCCACAGAGTGCACACTGTGTCGGAACCCGCT	450
Db	4412	TGTATCAAGCTGTTCCTGTGACAGTATACCAATATCAAGCTCTGTCTCCGAGCCAGAT	447
QY	4505	ATGGCAAGAGCTGGCAGTGAATTTCTCGGTGGGGGCACTGTGCTGCTTGAATGCACT	456

Db	4472	AAGGAAGAAATTGGTTCTGTAGTTTTCGCCGGCTCCATGCTCCGATTCCAGTGTGCACACC	4531
OY	4565	CCGGCTATGCCCTGACGGGTTGCCAGAGATCGAGTGCCTCCCTGTGCTTG366CCTTGG	4624
Db	4532	CGGGATACCTGCTTCAGGGTTTCCACGGCGCTCCACTGCAGATCCGTGCCCCAACCCCTTGG	4591
OY	4635	CCCAATGGAATGTCTCAGCGGCCACGTGTGTGTGTGCGGTGTGTGGAGGCAACTCCACAGC	4684
Db	4552	CACGTGTGAAGCAACGATATCCCAAGCTGTGTGTATCCCTGACGTGGCAATTTCACTCAAC	4651
OY	4685	GCAGGGGACCAATCCTGTCTCCCTGTGCTTCCAGAGCCGTACTCAACAGCCCTCAACTGTG	4744
Db	4652	GAAAGGTATACATCTGTCTCCCGGGCTACCCGTAGCCATACGGAACAACATTTGAACGTGA	4711
OY	4745	TGTGGAAGATGTGTCTCCCGAAGGCGCTGGCATTCAGATCCAAAGTTGTCAAGTTTGTGA	4804
Db	4712	TATGGAAGATCATATGTATTCGAGAGGCTGTGGAAATTCAGATCCAAAGTATCAAGTTTGTGCA	4771
OY	4805	CAGAGCAGAACTGGGACTCGCTGGAAGTATTTGATTTGTGTGAGATTAACCTGTAAACATATGC	4864
Db	4772	CGAGAGCAAACTGGGACTCCTTTAGATATCAAGATGTGTGGGATGTATGACCCGACCCAGAC	4831
OY	4865	TGGGAGTTTCTCAGGAACAACCGTGCCTCTTGTGAACGACCTCCACCAAGCTCT	4924
Db	4832	TGGGAAGCTTCTCAGGCAACACAGTACCGGCACTGTGTAAACAGTATCTTCCAAACCAACTCT	4891
OY	4925	ACCTTCAATTTCTACATATATCAAGTATCAAGCTATGTGACAGCTGCGTTCCACTTGGAGTAAACA	4984
Db	4892	ACCTGCATTTCTCAGTCTACATTTATGTGTGGAGCTGCTGTGTTTCCACTGGAAATACADA	4951
OY	4985	CGGTGGGCTGTAGCAGTGTGTCCGGAACCTGTGTGCCCCAGTAAACGGGTGTAAAGCTGGC	5044
Db	4952	CTGTATAGCTTGTGTGCATGCCAAGAACCAAGCCCTCCACAGCAACGATCAAAATCCGAG	5011
OY	5045	AGCGTACTTGTGTAAATATGTGTGTCTTTTCCAGTGTAGACCCGGAATATGCTCTCCAG	5104
Db	5012	ATCGGTAATGTGTGAACGATGTCTCTTCCAGTGTGAACCCGGGTACACCTTGACAG	5071
OY	5105	GCCACGCCCAATCTCTGCATATGCCCGGAACAGTGTGCGCGCATATGGAACCTACCTCTCCAC	5164
Db	5072	GCCGTCTCCCACTTTCTGTATGTCCAGGGAACGTTGCGCGTGTGAACATATCCGTCTCCC	5131
OY	5165	TCTGTATTGCAACAGTGTGGGGGAACAGTGTGAGAGATGAGAGGGGTGATCTTGAGCCCCG	5224
Db	5132	TGTGTATTGCAACCTGTGTGAGGGGACGCTGACACACTTGTGGTGTGTATCTGTAGCCCCG	5191
OY	5225	GCTTCCCAAGCAACTACCCCAAGTAAACATGAGCTGTCTGTGAAAATAGCACTGGCCGTTGG	5284
Db	5192	GCTTCCCAAGTTCTTACCCCAACACTTGAACCTGACCTGGAGGATCTCATTTACCATCG	5251
OY	5285	GCTTTGAGCTCACATCCAGTTCTCGAATTCTCCACCGAGCCCAACCCAGACTACATAG	5344
Db	5252	GCTATGGGACATATTCAGTTTCTGATTTTTCACCGAAGCTAATCATGATGATCTCTTGG	5311
OY	5345	AAATTCGGAATGTGCCCCCTATAGACACAGCCGATGTGGGAAGTTCAGTGTGAAGCGAGC	5404
Db	5312	AAATTTCAAAATGTACTTACACACACAGACCCCATGATTTGCAATTTAGCGGACGAGATC	5371
OY	5405	TTCCAGCTCCTCTCTCCACGTCTCCACAGAGACCAAGTATTTATTTCCACAGCAACACT	5464
Db	5372	TCCCGCGGCGCTGTGTGAGCAACACGATGAACCCCTCATCCACTTTTATGTATGACATT	5431
OY	5465	CCCAAGATTCGGCCAGAGATTCAAGCTGTGAGTATCAAGCCTTATGAACCTTCAA	5514
Db	5432	CGCAAAACCGGCAAGATTTTAACTTGTCTTCAAGATATGGAACAACAA	5481

RESULT 10
US-09-799-514-3
; Sequence 3, Application US/09799514
; Patent No. US20020065220A1
; GENERAL INFORMATION:

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: APPLICANT: Young et al.
: TITLE OF INVENTION: Immunoglobulin Superfamily Polynucleotides, Polypeptides, and A
: FILE REFERENCE: P7015P1
: CURRENT APPLICATION NUMBER: US/09/799,514
: CURRENT FILING DATE: 2001-03-07
: PRIOR APPLICATION NUMBER: PCT/US00/23662
: PRIOR FILING DATE: 2000-08-29
: PRIOR APPLICATION NUMBER: 60/152,248
: PRIOR FILING DATE: 1999-09-03
: NUMBER OF SEQ ID NOS: 19
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 3
: LENGTH: 2487
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-09-799-514-3

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Query Match	20.9%	Score 2122.4	DB 9	length 2487
Best Local Similarity	99.0%	Pred. No. 0		
Matches 2135, Conservative	0	Mismatches 21	Indels 0	Gaps 0

Oy	6238	GACATCCACAGGCGGATATCTCGAAGCCAGAGCTACCTGGAGCTATGCCAGTTCACAGCC	6237
Db	1	GACTCCACAGGCGGATATCTCGAAGCCAGAGCTACCTGGAGCTATGCCAGTTCACAGCC	60
Oy	6298	TGCTCTTGAGCGCTGAGAGTGGAGCCCGACATATATCTCTCCACAGTGGATATCTTC	6357
Db	61	TGCTCTTGAGCGCTGAGAGTGGAGCCCGACATATATCTCTCCACAGTGGATATCTTC	120
Oy	6358	CTCAGCCAGAGAACATATGATGAGCTTTTGATGAGTGTCCATCAGACAGAGTCTT	6417
Db	121	CTCAGCCAGAGAACATATGATGAGCTTTTGATGAGTGTCCATCAGACAGAGTCTT	180
Oy	6418	CTGCTGAAAGCCCTCAGTGGGAAATTACTACAGTCCCTCGATTTGACACAGCTCAAGCAAC	6477
Db	181	CTGCTGAAAGCCCTCAGTGGGAAATTACTACAGTCCCTCGATTTGACACAGCTCAAGCAAC	240
Oy	6478	TCTGTGTATCACTGCGTTGGTTCATCTGATACACGCCTACAAATCGAAGGGCTTCAAATCCGC	6537
Db	241	TCTGTGTATCACTGCGTTGGTTCATCTGATACACGCCTACAAATCGAAGGGCTTCAAATCCGC	300
Oy	6538	TATTCAGCCCTTACTGACGCTTGCCAGGGGCTCACTCCATGGCTTCATCTTAGCCAG	6597
Db	301	TATTCAGCCCTTACTGACGCTTGCCAGGGGCTCACTCCATGGCTTCATCTTAGCCAG	360
Oy	6598	ACACGACACCAAGCCCCGGGGGCTCCATACACTTTTGGCTGCAAGCGCGGCTACACCGCTGGT	6657
Db	361	ACACGACACCAAGCCCCGGGGGCTCCATACACTTTTGGCTGCAAGCGCGGCTACACCGCTGGT	420
Oy	6658	GGAACACAGCATGAGCATATCTGTACACCGGACCCCCAGGGCTTACACTCTGTGGAGCGAAGCC	6717
Db	421	GGAACACAGCATGAGCATATCTGTACACCGGACCCCCAGGGCTTACACTCTGTGGAGCGAAGCC	480
Oy	6718	ATCCCTCTCTGTCAAGCTCTTTCCTGTGGGCTTCTGAGGCCCCCAAGATGATGGTG	6777
Db	481	ATCCCTCTCTGTCAAGCTCTTTCCTGTGGGCTTCTGAGGCCCCCAAGATGATGGTG	540
Oy	6778	TTTGGCAAGAGATACACAGTGGGAACCAAGGCCGTGTACAGTGTGCAATGAAAGCTTACAC	6837
Db	541	TTTGGCAAGAGATACACAGTGGGAACCAAGGCCGTGTACAGTGTGCAAGAGGCTTACAC	600
Oy	6838	CTTCAGACAGGCGCTGAGGCCACTGACAGAGTGTCTGGACACAGGCTTATGGAGCAACCCG	6897
Db	601	CTTCAGACAGGCGCTGAGGCCACTGACAGAGTGTCTGGACACAGGCTTATGGAGCAACCCG	660
Oy	6898	AATGTCCCAACCAAGTGTGCTCTGTGACTTTGTCTGATGTCAATGATAGCATCAGCGTGGAG	6957
Db	661	AATGTCCCAACCAAGTGTGCTCTGTGACTTTGTCTGATGTCAATGATAGCATCAGCGTGGAG	720
Oy	6958	CATGGCCGATGAGAGGCTTATCTTTGAGACACAGTATAGTTCCAGGGCCAGCTGATGCTC	7017
Db	721	CATGGCCGATGAGAGGCTTATCTTTGAGACACAGTATAGTTCCAGGGCCAGCTGATGCTC	780

QY	7018	ATGTGGACCCCTGGCACTACATATACTGGCCAAAGGATATCCCTGTTCAGGCCAATGGC	70177
Db	781	ATTGTGATCCCTGGCTACTACTATATCTGGCCAAAGGGATATCCGCTGTTCAGGCCAATGGC	840
QY	7078	AAATGGAGCCCTGGGGACTCTACGCCCACTCCGATCATCTCTGTGGAGAGCTCCCG	7137
Db	841	AAATGGAGCCTGGGGACTCTACGCCCACTCCGATCATCTCTGTGGAGAGCTCCCG	900
QY	7138	ATTCCCCCAATGGCCACCGCATCTGGAAACACTGTCTGTCTACGGGGCAACGCCATCTTC	7197
Db	901	ATTCCCCCAATGGCCACCGCATCTGGAAACACTGTCTGTCTACGGGGCAACGCCATCTTC	960
QY	7198	TCCTGCATATTCGGATACACACTGGGTGGCTCCAGAGTGCGGTGAGTGGATGGCCAAATGGG	7257
Db	961	TCCTGCATATTCGGATACACACTGGGTGGCTCCAGAGTGCGGTGAGTGGATGGCCAAATGGG	1020
QY	7258	CTCTGGATGGCTCTGGAGTCCGCTGCTTGGTGGACACTGTGGACTCTTGAGCCCATY	7317
Db	1021	CTCTGGATGGCTCTGGAGTCCGCTGCTTGGTGGACACTGTGGACTCTTGAGCCCATY	1080
QY	7318	GTCAACGGACACATCAATATGGGGAGAACTAACACTACCGGGGCAAGTGTGTACCAATGC	7377
Db	1081	GTCAACGGACACATCAATATGGGGAGAACTAACACTACCGGGGCAAGTGTGTACCAATGC	1140
QY	7378	AATGCTGGCTTCGCTGTGATGGCAATGTCTGTGCGCATCTGCACAGAGATCATCACTGG	7437
Db	1141	AATGCTGGCTTCGCTGTGATGGCAATGTCTGTGCGCATCTGCACAGAGATCATCACTGG	1200
QY	7438	TGGGGCAAGACCCCTTCTGTGTGGCAATTAACCTGTGGACACCCAGGCAACCTGTCAAC	7497
Db	1201	TGGGGCAAGACCCCTTCTGTGTGGCAATTAACCTGTGGACACCCAGGCAACCTGTCAAC	1260
QY	7498	GGCCTCACTCAGGGTAAACCAATTAACTCAACGATGTGTGCAAGTTTGTGTGCAACCT	7557
Db	1261	GGCCTCACTCAGGGTAAACCAATTAACTCAACGATGTGTGCAAGTTTGTGTGCAACCT	1320
QY	7558	GGGTATATAGGCTGAGAGGGGCTGTATAGTTCCTTAATGCTGTGGCAAGCGGCAATGGAGTAC	7617
Db	1321	GGGTATATAGGCTGAGAGGGGCTGTATAGTTCCTTAATGCTGTGGCAAGCGGCAATGGAGTAC	1380
QY	7618	ATGTGCCCACTGTGAGAAATCATCAACTGTACAGATCTGTGACACCAAGAAATATAGTGT	7677
Db	1381	ATGTGCCCACTGTGAGAAATCATCAACTGTACAGATCTGTGACACCAAGAAATATAGTGT	1440
QY	7678	CGTCAAGTTCACGCCAGGCGCCCGACAGGTTACGTTTCGGCACCACTGTGTCTTAACCGG	7737
Db	1441	CGTCAAGTTCACGCCAGGCGCCCGACAGGTTACGTTTCGGCACCACTGTGTCTTAACCGG	1500
QY	7738	TGCAACCAAGGACTTCTAATCTCTGTGGGACCCCAAGTGTCAAGCTGCGCAAGGGAGATGGCAAC	7797
Db	1501	TGCAACCAAGGACTTCTAATCTCTGTGGGACCCCAAGTGTCAAGCTGCGCAAGGGAGATGGCAAC	1560
QY	7798	TGGGACCGTCCCGCCCCCAAGTGTCTTGGTGTCTGTGGCCATCCGGGCTCCCGGCT	7857
Db	1561	TGGGACCGTCCCGCCCCCAAGTGTCTTGGTGTCTGTGGCCATCCGGGCTCCCGGCT	1620
QY	7858	CACCTCCAGATGTCTGGAGACAGTTAATCTGTGGGACCAATGGTGGCGGTCACTGTGATTC	7917
Db	1621	CACCTCCAGATGTCTGGAGACAGTTAATCTGTGGGACCAATGGTGGCGGTCACTGTGATTC	1680
QY	7918	GGCAGACGTAATCTGTGTGGAGAAACAGCAACCGCATGTGTGGGCTGGATGTGACACTGGACT	7977
Db	1681	GGCAGACGTAATCTGTGTGGAGAAACAGCAACCGCATGTGTGGGCTGGATGTGACACTGGACT	1740
QY	7978	GGCTCCCTCCCTCACTGTCAAGAAACCAAGGTGTGGAGATTTGCGGTGACCTCTGGGATCCCG	8037
Db	1741	GGCTCCCTCCCTCACTGTGTCAAGAAACCAAGGTGTGGAGATTTGCGGTGACCTCTGGGATCCCG	1800
QY	8038	GCTCATGGCAATCCGTTTGGGGGACAGCTTTGATTCAGGCACTGTGATGTGGCTTCACTGTG	8097
Db	1801	GCTCATGGCAATCCGTTTGGGGGACAGCTTTGATTCAGGCACTGTGATGTGGCTTCACTGTG	1860
QY	8098	GAAAGTCGCACTGTCTCCGGGATCGTCAAGGCGCACTGTCAAGCCAAATGGCTGTGGG	8157

[illegible]

QY 283 AGCTCACTTCACTGCAACGAGGCTATGACCTGCAAGGGCTCCAGCGATCACTCT 342
 DB 703 AATGACAGCTTTCACTGAGGACAATTAAGTCTCCAGGATCTAAAGACATCACTCT 762
 QY 343 ATGAAGTGAAGGACATGTTTGGCGCTGAGACGACACAGGCGAGTCTGCGAGCCGC 402
 DB 763 CAGAGAGTTACAGAGACGCTGCTGTTGAGTGAACACAGGCGCATCTGCGAGCAGA 822
 QY 403 ATGTGTATGCCACCTTGAAGCCCTCTGCGCATCATCACTCCCAATTTCCCAATT 462
 DB 823 ACATGTGATTCATCTGCTGGGCGCACGCGCTCATCTCCCAATTTATCCGTT 882
 QY 463 CAGTATGACAGATGACACATGCTGTGTGATCATCAAGCACTCAACCCCTCAAGTG 522
 DB 883 CAGTATGAGATTAATGACACATGCTGTGTGATCATCAAGCACTCAACCCCTCAAGTG 942
 QY 523 ATCAAGCTCGCTTTGAGGAGTTTGAATTTGAGAGGGGCTATGACACCTGACGCTG 582
 DB 943 ATCAAGCTCGCTTTGAGGAGTTTGAATTTGAGAGGGGCTATGACACCTGACGCTG 1002
 QY 583 GATGTGTGATGAGAGGACCAAGAGACATTTCTTACATGCTTCAAAATGCTGACGT 642
 DB 1003 GATGTGTGAGAGGAGGAGACACAGATGCTTGTACGTG-CTCACGGATTCAGTGT 1061
 QY 643 GACAGCCCTCACACCCAGGCTCGCATCCAGAGAGCATGCTGGGAGCATCTGAGAG 702
 DB 1062 TCTTGACTTCA-----TTGTGACATGAGACACAGATGCTGACGT 1111
 QY 703 CAGAAATGACCTGTACTGAGATCTGTGCTGACATTAAGCATTCAGATGCAAGTCAAGT 762
 DB 1112 CGGATGATGACATGTGCTCACTGAGT----- 1138
 QY 763 TCAGTGAAGAGTCTCAAAAGCTTCTAATGCTGTGGAATTTGTTGCTCTGAGAGAG 822
 DB 1139 -----TTAAAGCTGTTTACCAAGAA 1158
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 QY 883 CGGTTTCAACGAGTACACATCTCAAGTTTGAAGTTCAGCGCGCTTTGAGCTGTGGGA 942
 DB 1219 AGTTTCTCCATGAGATACATCACTTGAATGCGCGCGCTTTGAGCTGTGGGG 1278
 QY 943 CAGAAAGCATCACTGAGCAAAAGATTAACCAATGCTGCGCTTAAGAGCGAGGCTGCG 1002
 DB 1279 GAGAGAGTTATCCGTCGACAGAACATCAAGTGTCTGGCAACAGGCGAGCTGTGTA 1338
 QY 1003 TTCTCTGCTTCTTCAACTTACACAGCGCTGTGGGTTGTCTCTCTCCCACTACCA 1062
 DB 1339 TTTTCAATGTTTCTTCAACTTACAGGATCATCTGGGATTAATCTGTACCAAAATTAACA 1398
 QY 1063 GAGAGCTATGAGCAACCACTTCACTGTGTGCTCAATCTGAGCGAGCTGAGAGCGCG 1122
 DB 1399 GAGGAATATGAGAAACAATGAATGCTGTGTGATTAATCTCGAGGAGAGAACTCA 1458
 QY 1123 ATCAAGCTCGCTTCAACGACATTAAGTGTGAGCTCAAGTTTCCGTCATCAAG 1182
 DB 1459 ATTCACTTAATCTTAAATGATTTGATGATGAGCTCAATTTTCTCTCGGATCAAG 1518
 QY 1183 GATGAGGACCAACCGCGAGGCGCTCTGAGGACCTTCTCAGAAACCAAGCTTCCCTCC 1242
 DB 1519 GATGATGAGCATTTCTGACATAACGATCTGGGATCTTTTCTGAGCATGAGAGCTTCC 1578
 QY 1243 TCCATCAACAGAGTGGCCAGTGGCCGCTCTGAGTTCCAGCTGACATCAACAGG 1302
 DB 1579 CAGCTGGCCAGAGTGGGCAATAGTTCGCTTGAATTCAGTCTGACCAATTCACACTACT 1638
 QY 1303 AAGAGGGGCTTCAACATCACTTTTACCACTTCCGACACAAAGAGGCGGAGTCTGAGC 1362
 DB 1639 GCGAGAGGTTCAACATCACTTACACATTTGGGTGAAATGATGACATGATCTGAGC 1698
 QY 1363 GTTCACTAATATGCAACGATTTGGGAGACAGCTTCAAGCTGGGAGCTTCATCTCTTC 1422

DB 1699 ATTCTATTAACGACACAGCTTTTGGTGAACAGTTTCTACTCGGAGCTCGCTTCTTTC 1758
 QY 1423 CTCTGTATGAGAGCTTCTTGGGACCTAGAGCTCAGAGCACTACCTGCGCTGAG 1482
 DB 1759 CACTGTATATGAGCTTGTGCAAGACCCAGAGATCCAGATCAATACCTGACATACGCA 1818
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 DB 1819 GAGGAGACCTGTGTGAGACTCAACCTGTCCCGCTGTGAACTCATGTGTGAGCAT 1878
 QY 1543 CTGACTTCCGACAGGCAACATCTCTCTTCCGAGCTGGCTGTCTTCAAGAGATCC 1602
 DB 1879 CTGACAGCTTCAAGCGGAGCATTTTGTCTCTGATGAGCCAGAGATTTTAAGATCT 1938
 QY 1603 TTGAGCTGTGCTGGGATTTGAGGCGCCAGCGGCTAACCCCATCAAAATCACCTTGCAC 1662
 DB 1939 TTACATTTGAAATGAAATTTGAAGCAAAACAGGCACTCATCAAAATTAACCTTTGAC 1998
 QY 1663 AGATTTCAAAACCGAGTCACTATGACACCTGGAATGACGATGAGCGGAGCTTACTCA 1722
 DB 1999 AGATTTCAAGAGAGTCAATTAATGACACCTTGAAGTCAAGATGAGCGGAGCTTCC 2058
 QY 1723 GCGCTTGTATCGGAGTTTACACAGGACCCAGGTTCCCAATTTCTCATCAGACCAAC 1782
 DB 2059 TCCCACTGATCGGCGAGTACACAGGACCCAGGACCCCAAGTTCTCATACAGACCGGG 2118
 QY 1783 AACCTAACCTAACCTCTCTCTTCAACGACAAAGATGACATCGGACATCGGCTTCACTC 1842
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 QY 1843 CGCTATGAGACTATTAACACTGACAGACCACTGTGTGATTCAGAGATTCAGATTAAT 1902
 DB 2179 CACTATGAGAGTGAAGCTTGAAGTTCGATTCGCTTGAAGCCGAGCATCTCTGTGAAC 2238
 QY 1903 GGAAGGCTCATGAGGAATGACTTCTACGTGGGCGGCTGTGATCTTCACTGTGATCTCG 1962
 DB 2239 GGCATCGCCACGCTGAGACATTTGGCATCAGTTCACAGTATTTCACTGTGATCTCG 2298
 QY 1963 GGCCTAACATTAATGAGCGGAGGACCTCTGAGTGTGAGCCCACTTCAAGTGAAGCCGG 2022
 DB 2299 GGTATACACTAATGATGACAGAGCCCTGTCTGTGAGAGGAAACACAGTGAACACAC 2358
 QY 2023 GCGCTGCCAGTTGTGAAGCTCTGTGTGAGCTTCAATCAAGGCTCCAGTGAACCATC 2082
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 QY 2083 TTGTGCGAGGTTCTCTGACTTCTACCCCAACAATTTGAATGACATGATGATGAA 2142
 DB 2419 CTCTCTCTGAGTTTCAAGATTTTATCAAACTCTTAACCTGACGAGCAATGAA 2478
 QY 2143 ACATCTATGAGGAGGAGTGTCTTCACTTCAACCTTCAACCTTGAAGAGTGGCAT 2202
 DB 2479 GTGTCTATGAGGAGGAGGATTAATGATCTTCAACCTTCAACCTTGAAGAGTGGCAT 2538
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 DB 2539 GACTATTTACTGATCAAGAGATGAAATTTTCCGAGCCGCTGAGGAGCTCAACCCGG 2598
 QY 2263 TCTGAGGCTGAGCTCCCATAGCGCTGGGCTTAATGAGCACTTCACTGAGGAGTGGC 2322
 DB 2599 TCGGTGTGCTTCAATGATCAAGGAGGCTGTGTAAGAACTTCACTGAGGAGTGGC 2658
 QY 2323 TTCACTCTGATTTTCTCATGATGATGAGATTTCAACATCACTTCTCAGAGTACAC 2382
 DB 2659 TTTATATAGACTTCTCAATTTGATGAGGAGCTTCAATCACTTCTCAGAGTACAC 2718
 QY 2383 TTGAGAGCTGTGAGAGAGCGAGGCTCCAGCTTACAGCATCCGAGAGGCTTGAAGTT 2442
 DB 2719 CTGAGAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2778
 QY 2443 GCGGTGGGAGACCTTGAACCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2502

Db 2779 GGTGTGGAGACTCTCTGACGTTTCCTGCTGCGGATATGTTAGAAAGTGCACC 2838
 QY 2503 CGCATCAGCGCTGGGGGGGACAGCGCGCTGTGGAGCTCGCTCGCAAGGTGTT 2562
 Db 2839 AAGCTTACCTGCTGGGTGGGGGCGCGGTGTGGAGTGCACCTCGCCAAAGGTGTG 2898
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 Db 2899 GCGGATGTGGAGACAGTGTCAAGGAAATGAAGAAACATTAATGTCTCCAAATTTTCCA 2958
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 Db 2959 TCCAAATTAATATATTAACCATGAGTATCTATTAATAATGAACAAGCCGCAAGGGC 3018
 QY 2683 ATTCACTGAAAGCCAGGGGATTCGAATCTCCGAAAGAGATGCTCAAGGTTTATGAT 2742
 Db 3019 ATCCACCTTAGAAGACAGAGAGCTTCAGCTGTGTAAGAGAAATCTTAAAGGTATATGAT 3078
 QY 2743 GGCACAAACAACTCCGCGCTTGTGCGGAGTTTATAGCCATTCTGAGATGAGGGGTG 2802
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 QY 2863 AGAAGGGCTTTGAATCTGACCTTTTCCAGCTTTGAATCTCAATATGTGAGACCCAGGA 2922
 Db 3199 GACCAAGGTTTGAATCTGACCTTTTGAATCTGATTTGAATGTGAGATCCGGGG 3258
 QY 2923 ACCCCCAAGTTGGCTACAAAGTTTCAATGATGAAGTCAATTTTGCAGGAGCTCGTGC 2982
 Db 3259 ATCCCTAACATGAGGCTATGAGATCCGTGATGAAGGCACTTTTCCAGACATGATGTTG 3318
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 Db 3319 TACAGTTGCAACCCGGGGTACGCCATGATGAGCAACACCTGACCTGTTTGAAGTGA 3378
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 Db 3379 GACAGAGAGTGTGGGACAAACCACTACCTTCTGTGATACCGGAATGTGTGTGACAGATC 3438
 QY 3103 AGAGAGAGGTGTGCGGGGACGAGTGTCTGACCCCGGGTATCCAGCTCCCTATGAACAAT 3162
 Db 3439 CATGCGCCCAATCAGAGAGAAATATTTGCTCCCTGCTATCCAGCTCCGATGCAACAC 3498
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 Db 3499 CTCACATGCACTGGAATTAATAGAGGAGAGCCAGAAAGCATTAAGCTTCATTTCTAT 3558
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 QY 3283 GGGGTTCTGTGAAAGAGTGAATGGCCGCGCCCTGCCAAGGACCTGCAATACCACTTC 3342
 Db 3619 GACATCTGTGTAAGAGTGAATGGTGTGCTCGCCCTTCGAGGAGACATCCACACACTTC 3678
 QY 3343 AACTCGGTGTCTCTGAGTGTGACAGTGTCTTTCACAGAGAGAGGGCTTGGCAAT 3402
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 QY 3403 CAATTTTC 3410
 Db 3739 CAGTTCTC 3746

RESULT 13
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 ; FEATURE:
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 ; OTHER INFORMATION: Incyte ID No: 6813464CBI
 ; US-10-398-037-69
 Query Match 13.5%; Score 1371.6; DB 17; Length 2387;
 Best Local Similarity 90.5%; Pred. No. 0;
 Matches 1510; Conservative 0; Mismatches 74; Indels 84; Gaps 1;
 QY 1 ATGGCGGGGCGCCCTCCCGCGCTTGTCTGCTGCTTGTGAGTTTATCTCAGACTGCTG 60
 Db 1 ATGGCGGGGCGCCCTCCCGCGCTTGTCTGCTGCTTGTGAGTTTATCTCAGACTGCTG 60
 QY 61 GCTAGCAATCAGGACACTTCCTGGGCGTATGAGACCTTCGAGCTAGTCAAGAAACAATT 120
 Db 61 GCTAGCAATCAGGACACTTCCTGGGCGTATGAGACCTTCGAGCTAGTCAAGAAACAATT 120
 QY 121 GAGTTGAATCTCGAGGTGTGAAGCTGATGCCAGCAAGACAAAGCCAGAGAGCTCT 180
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 Db 181 GTGTTAATCAGATTGGTGTGTGTCCCAAGGACATAATATATGTGTGTCCAGACCTTGGCATACC 240
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 QY 301 AAGAGGGCTATGACCTCGAAGGTTCACAGCCGATACCTGTATGAATGAGCGGACATG 360
 Db 301 AAGAGGGCTATGACCTCGAAGGTTCACAGCCGATACCTGTATGAATGAGCGGACATG 360
 QY 361 TTGTGCGCTGAGAGCAGACAGGCGCAGTCTCCGAGCCCGGATGTGTATGCCACCTT 420
 Db 361 TTGTGCGCTGAGAGCAGACAGGCGCAGTCTCCGAGCCCGGATGTGTATGCCACCTT 420

Db	300	GAAAGCTGGCAGGGCTACTTGGTGAATGAATGTGTGCTTTCCAGTGTGAGCCGGGATA	359
OY	5094	TGCCCCAGGAGCCACGGCCACATCTCTGTGATGTCGCCGGAACAGTGGCGGATGAACTA	5153
Db	360	TGCCCTCCAGGGCCACGGCCCAATCTCTGTGATGCCCGGAACAGTGGCGGATGAACTA	419
OY	5154	CCCTCTCTCACTCTGTATTTGCACAGTGTGGGGGAAACAGTGGAGGAGATGAGGGGGTGAT	5213
Db	420	CCCTCTCTCACTCTGTATTTGCACAGTGTGGGGGAAACAGTGGAGGAGATGAGGGGGTGAT	479
OY	5214	CCTGAGCCCCGGGCTTCCAGGCAACTACCCAGTAACATGGACGTCTCTGGAATAATAGC	5273
Db	480	CTTGAGCCCCGGGCTTCCAGGCAACTACCCAGTAACATGGACGTCTCTGGAATAATAGC	539
OY	5274	ACTGCCCCGTGGGCTTTGGAGCTCAATCTCAGTTCTCTGAATCTTCCACCGAGCCCAACA	5333
Db	540	ACTGCCCCGTGGGCTTTGGAGCTCAATCTCAGTTCTCTGAATCTTCCACCGAGCCCAACA	599
OY	5334	CGACTCACTAGAAATTCGGAAATGGCCCCCTATGAGACCAAGCCGATGATGGAGATTGAG	5393
Db	600	CGACTCACTAGAAATTCGGAAATGGCCCCCTATGAGACCAAGCCGATGATGGAGATTGAG	659
OY	5394	TGGAAGGAGGCTTCCAAAGCTCCCTCTCTTCCACGCTCCACGAGACCAACCGGTATTTCCA	5453
Db	660	TGGAAGGAGGCTTCCAAAGCTCCCTCTCTTCCACGCTCCACGAGACCAACCGGTATTTCCA	719
OY	5454	CAGCGACCACTCCCGAATTCGGACCGAGATTCAAGCTGAGATATAGGCTTATGAATTTCA	5513
Db	720	CAGCGACCACTCCCGAATTCGGACCGAGATTCAAGCTGAGATATAGGCTTATGAATTTCA	779
OY	5514	AGAGTGCCCAAGCCAGAGCCCTTTTGGCAATGGCAATTTGAGAGGAGCTGAGCTAACAGT	5573
Db	780	AGAGTGCCCAAGCCAGAGCCCTTTTGGCAATGGCAATTTGAGAGGAGCTGAGCTAACAGT	839
OY	5574	GGGACAAATCAGTACCTTCCAGTGTCTCCCGGGGATATGAATTTGACTGGCCACCTGTCT	5633
Db	840	GGGACAAATCAGTACCTTCCAGTGTCTCCCGGGGATATGAATTTGACTGGCCACCTGTCT	899
OY	5634	CACGTGTCAACATGGCAGCAACACCGGAATGGGAACACCCCTGTGCCAAGTGTGAAGTCC	5693
Db	900	CACGTGTCAACATGGCAGCAACACCGGAATGGGAACACCCCTGTGCCAAGTGTGAAGTCC	959
OY	5694	TTGTGGCGGGAACATCACTTCTTCCAAACGGGACGTGTGTACTTCCCGGGGTTCCCTAGCC	5753
Db	960	TTGTGGCGGGAACATCACTTCTTCCAAACGGGACGTGTGTACTTCCCGGGGTTCCCTAGCC	1019
OY	5754	GTACTCCAGCTTCCAGGACTGTGTCTGGCTGATCAACGTGCCATTTGGCCATGGCGTCCG	5813
Db	1020	GTACTCCAGCTTCCAGGACTGTGTCTGGCTGATCAACGTGCCATTTGGCCATGGCGTCCG	1079
OY	5814	CCTCAACCTCAGCCGCTGTGAGACAGAGAGCCCTGTGGAATTTCAATCAATCTGGGATGG	5873
Db	1080	CCTCAACCTCAGCCGCTGTGAGACAGAGAGCCCTGTGGAATTTCAATCAATCTGGGATGG	1139
OY	5874	GCCACAGCAAAACAGCAGCAGGCTTGGGCTTTCAACCCGAGCATGSCCAAGAAACAGT	5933
Db	1140	GCCACAGCAAAACAGCAGCAGGCTTGGGCTTTCAACCCGAGCATGSCCAAGAAACAGT	1199
OY	5934	GCAGAGTTCAATCAACAGAGTCTCTGCTCAAGTTCCACCGTATGACGCCACAGGGGGGAT	5993
Db	1200	GCAGAGTTCAATCAACAGAGTCTCTGCTCAAGTTCCACCGTATGACGCCACAGGGGGGAT	1259
OY	5994	CTTGCCCAATGCTTCTCCGCTTA 6017	
Db	1260	CTTGCCCAATGCTTCTCCGCTTA 1283	

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TITLE OF INVENTION: INTRACELLULAR SIGNALING MOLECULES
FILE REFERENCE: PF-0827 USN
CURRENT APPLICATION NUMBER: US/10/399,455
CURRENT FILING DATE: 2003-04-14
PRIOR APPLICATION NUMBER: PCT/US01/32090
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PRIOR APPLICATION NUMBER: US 60/244,723
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PRIOR APPLICATION NUMBER: US 60/252,622
PRIOR FILING DATE: 2000-11-22
PRIOR APPLICATION NUMBER: US 60/255,622
PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PERL Program
SEQ ID NO 31
LENGTH: 2609
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No: 7473630CBI
US-10-399-455-31

Query Match          7.7%, Score 783.6; DB 17; Length 2609;
Best Local Similarity 62.1%; Pred. No. 6,2e+22;
Matches 125; Conservative 0; Mismatches 764; Indels 3; Gaps 1;

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Qy      3143 CAGCTCCCTTAGAACACAAATCTCAACAGTCATCTGAGCACCATGAGAGAGGCGGGCTGCA 32022
Db      637 CTTTTCCTATAGCAATATACCTGCGTTGCAATGTGAATGATTTAGAGTAAATCTTGAATA 696
Qy      3203 CCAATGGGCTACACTTCCTGCTGTTTGAACACAGAGAGGTTCAACGACGTGCTGGCATCT 32622
Db      697 TTGCAGCTTCAGATTTCTCTCTTTGTAACGGAAGCATCACATGATATATCTCCGAGCT 756
Qy      3263 GGAATGGGCTCTGTGAGAGAGCGGGTTCCTGCTGAACGACGTGAGTGGCCCGGCGCTGCCCA 33222
Db      757 GGGAGCGGTCCACGAAATATATATGCTTTTAAAGAAATTAATGATCTCTTAATTCCTG 816

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QY 3323 AGGACCTGATAGACCTTCAACCTCGTCGCTCGAGTTGACACTGACTTCTTACCA 3382
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 QY 3383 GCAGACGGGCTTTGCCATTCAATTTTCAAGTGTCCACAGCAACGTCCTGCAATGACCTG 3442
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 DB 937 GGGTCCCACTGAATGGAGTCTGAATGGAGATGGAAGAACTTGGGGACACTGTGTGT 996
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 DB 1237 GTTTTAACTGAGGACCAAACTATGACTTCTCATATCTATGATGACAGCACTAATTA 1296
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